FIG. 1

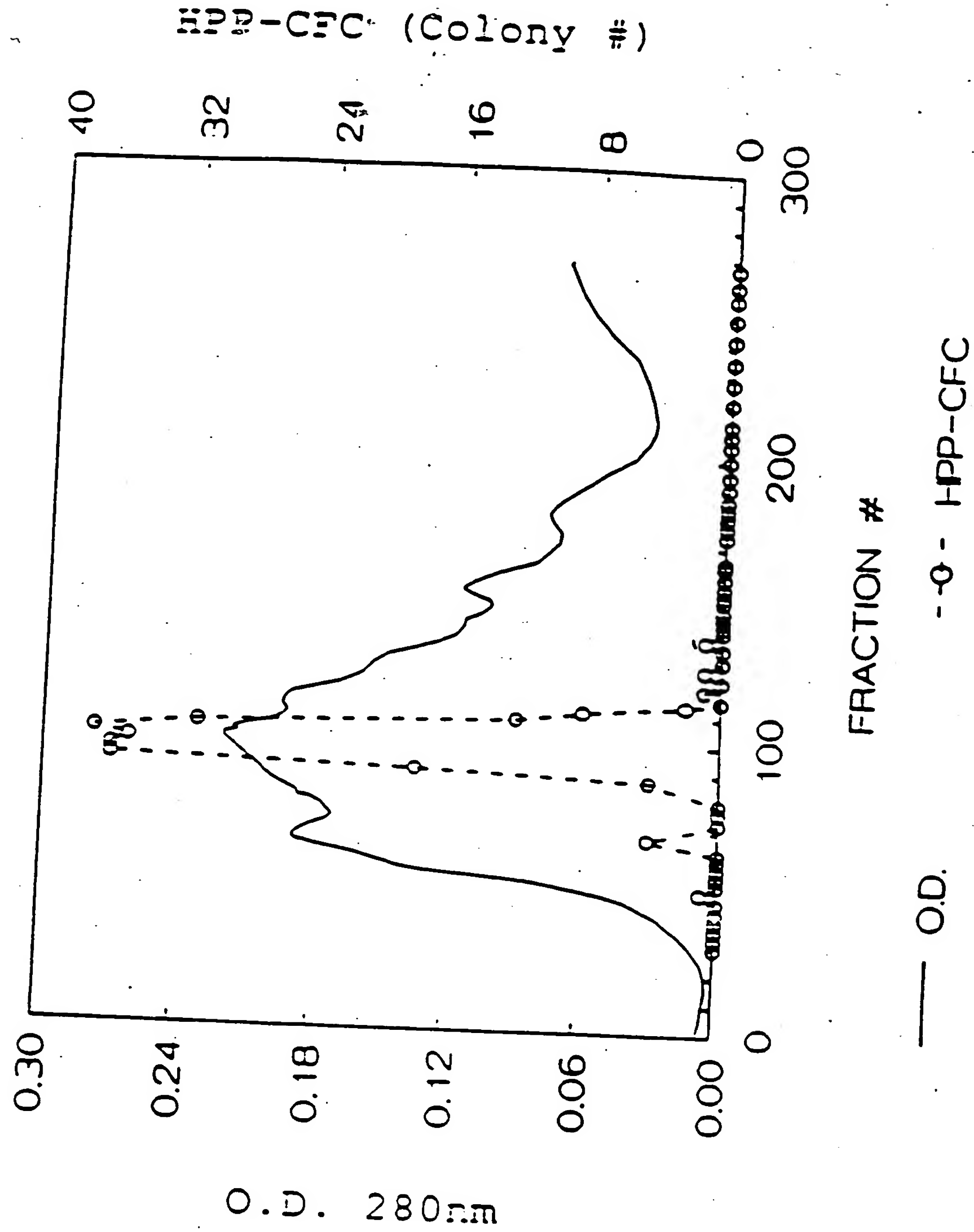

HPP-CFC (Colony #)
40
32
24
16
8
0
0.30
0.24
0.18
0.12
0.06
0.00
O.D. 280nm
0
100
200
300
FRACTION #
O.D.
HPP-CFC

FIG. 2

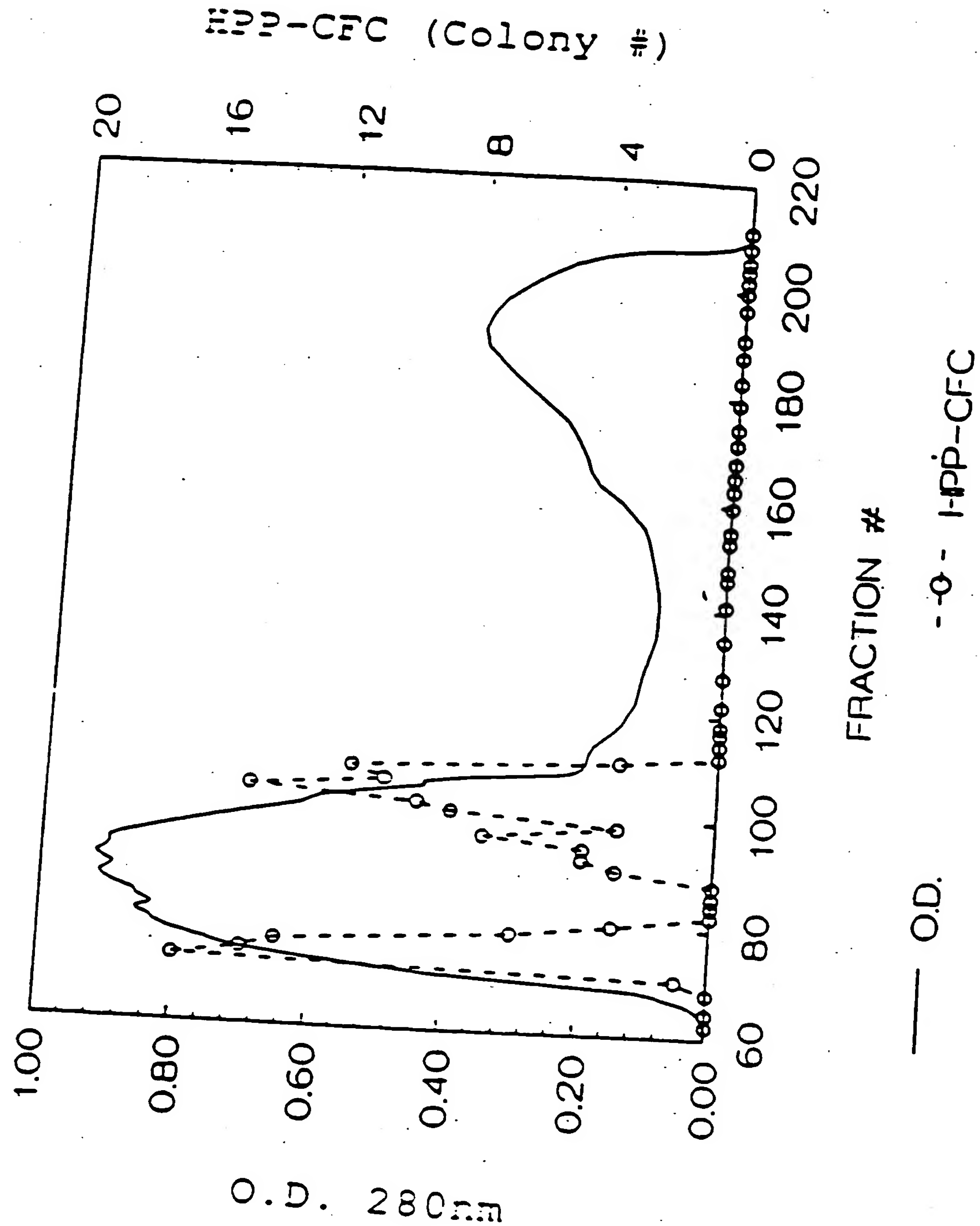

HPP-CFC (Colony #)
20
16
12
8
4
0
220
200
180
160
140
120
100
80
60
FRACTION #
- -o- - HPP-CFC
— O.D.
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm

FIG.3

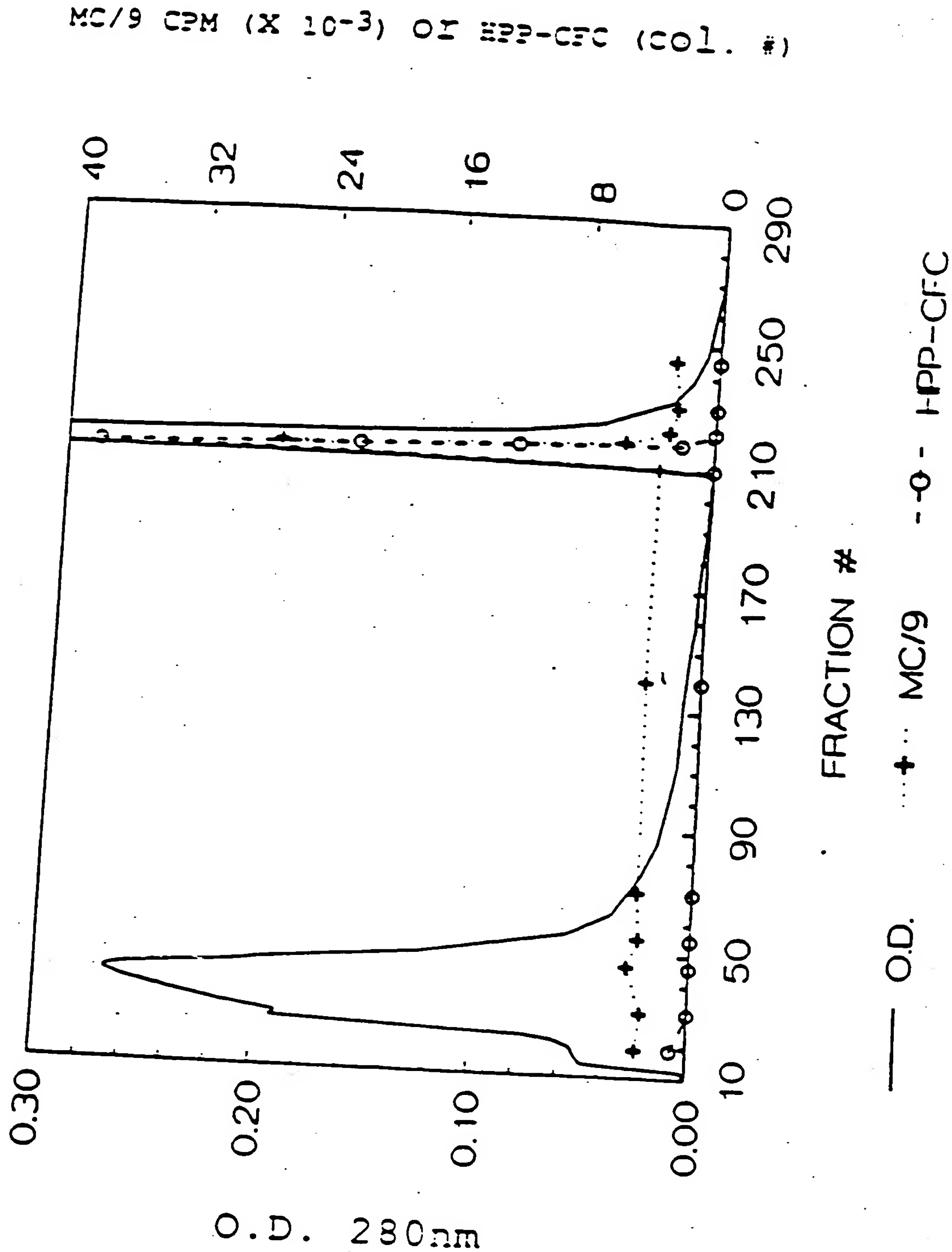

MC/9 CPM (X 10-3) or HPP-CFC (col. #)
40
32
24
16
8
0
290
250
210
170
130
90
50
10
0.30
0.20
0.10
0.00
FRACTION #
— O.D.
··+·· MC/9
-o- HPP-CFC
O.D. 280nm

FIG. 4

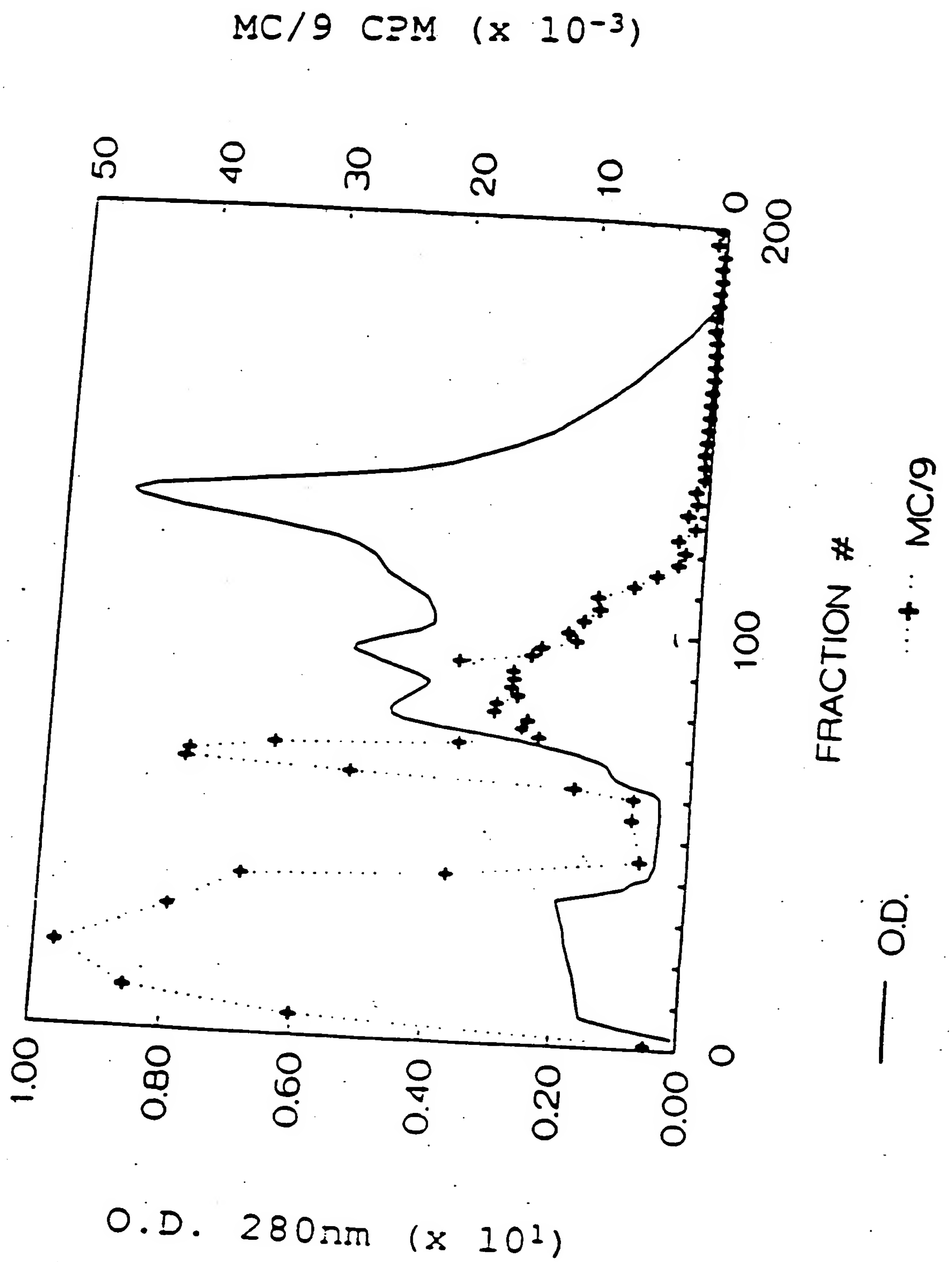

MC/9 CPM (x 10⁻³)
50
40
30
20
10
0
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm (x 10¹)
0
100
200
FRACTION #
O.D.
MC/9

FIG.5

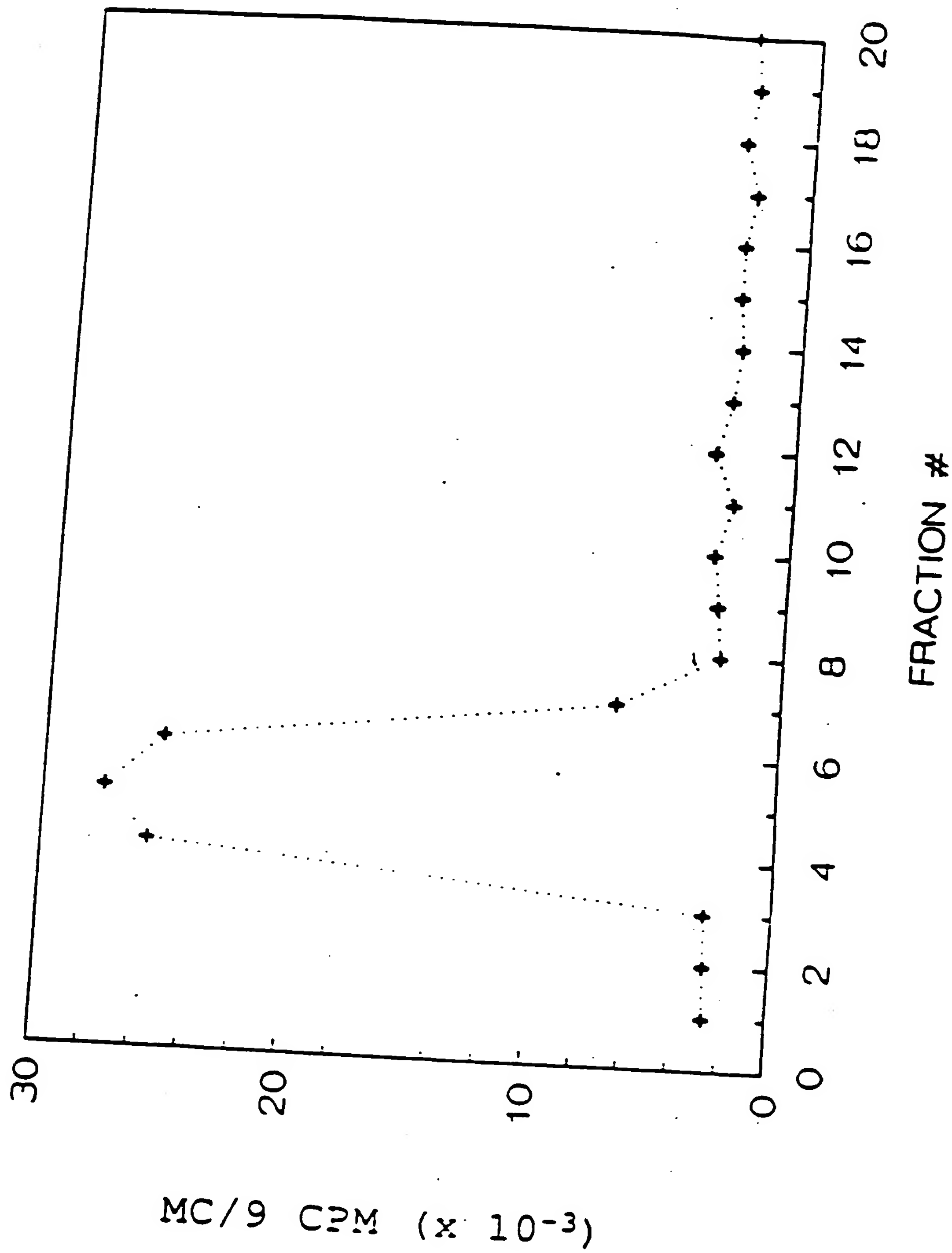


FIG. 6

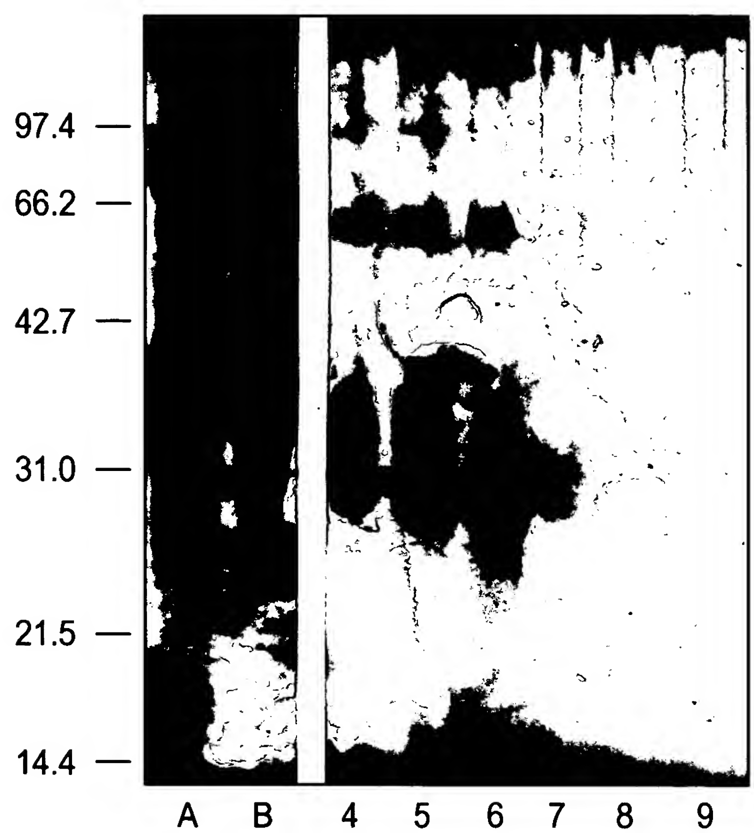


FIG.7

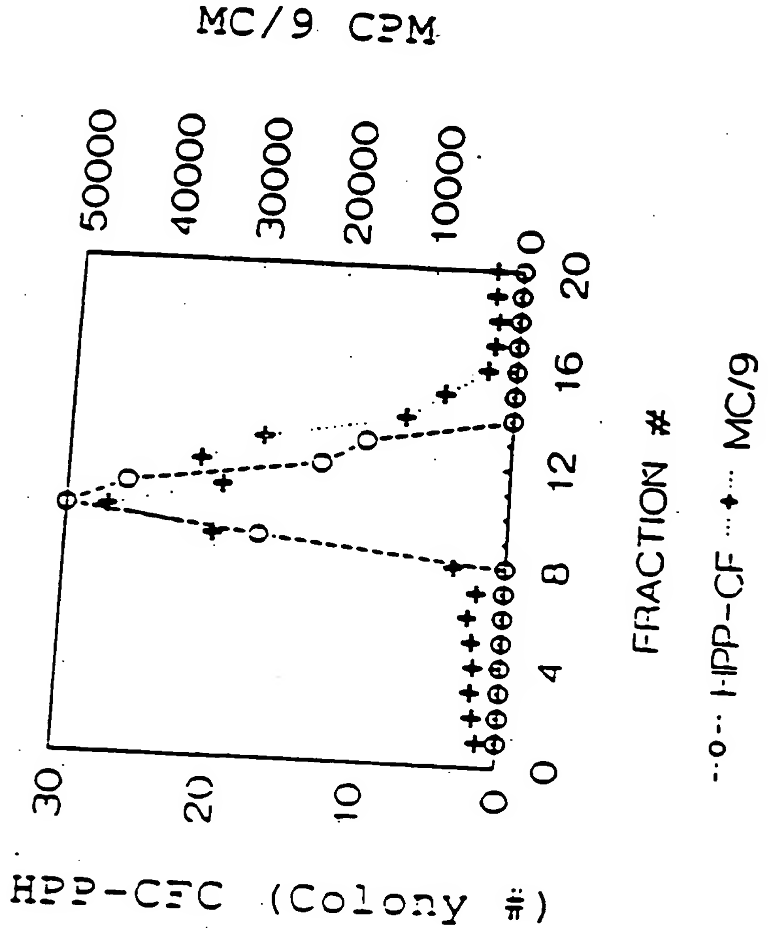

MC/9 CPM
50000
40000
30000
20000
10000
0
30
20
10
0
0
4
8
12
16
20
FRACTION #
--o-- HPP-CF ...+... MC/9
HPP-CFC (Colony #)

FIG. 8

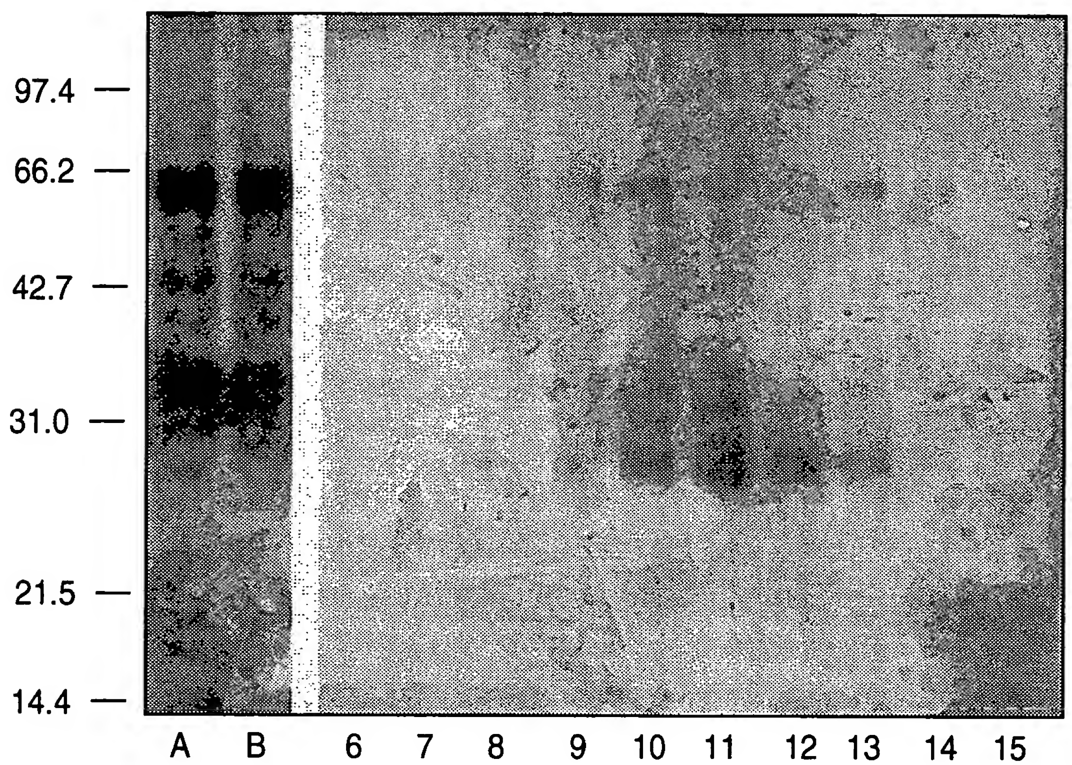


FIG. 9

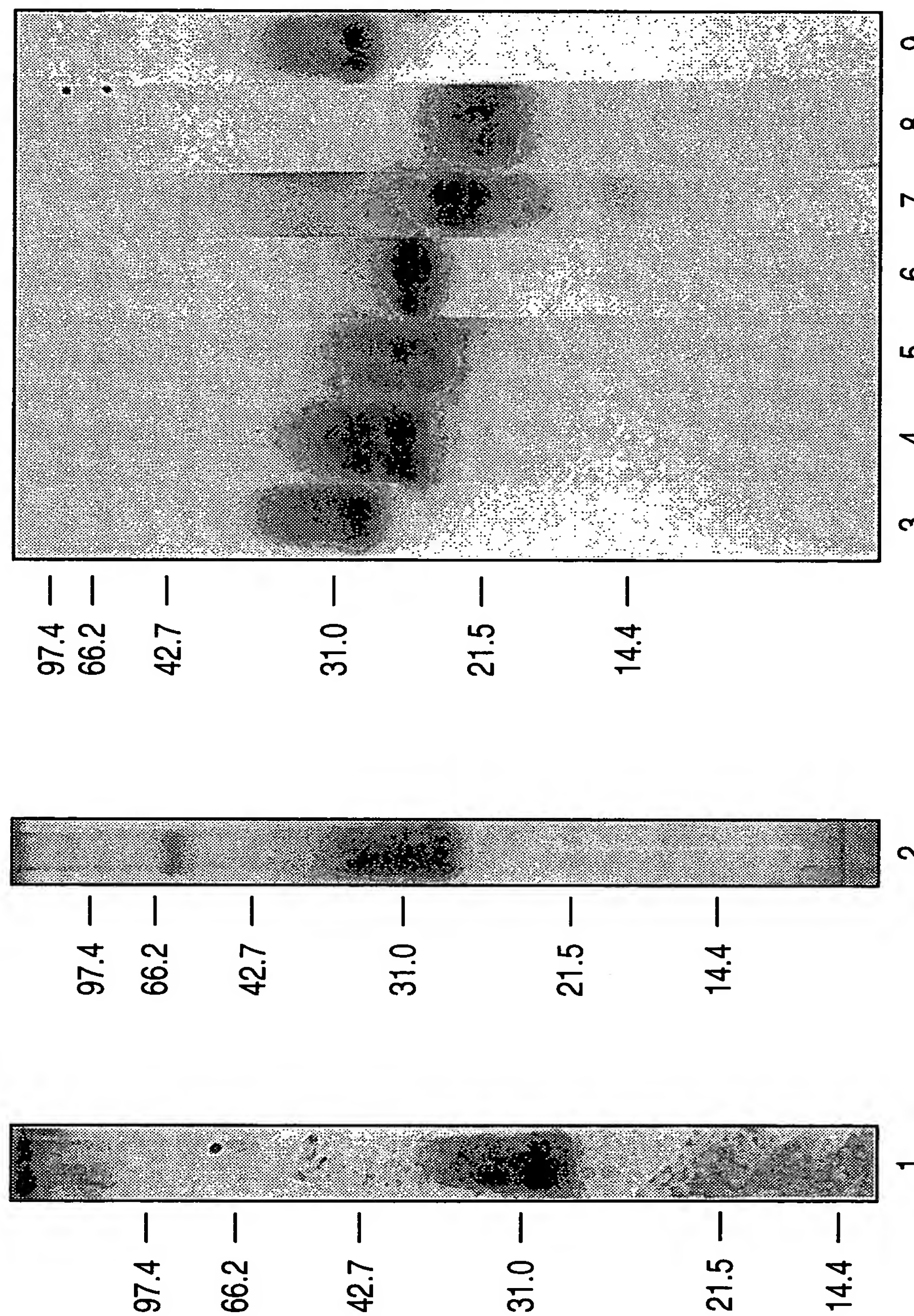


FIG.10

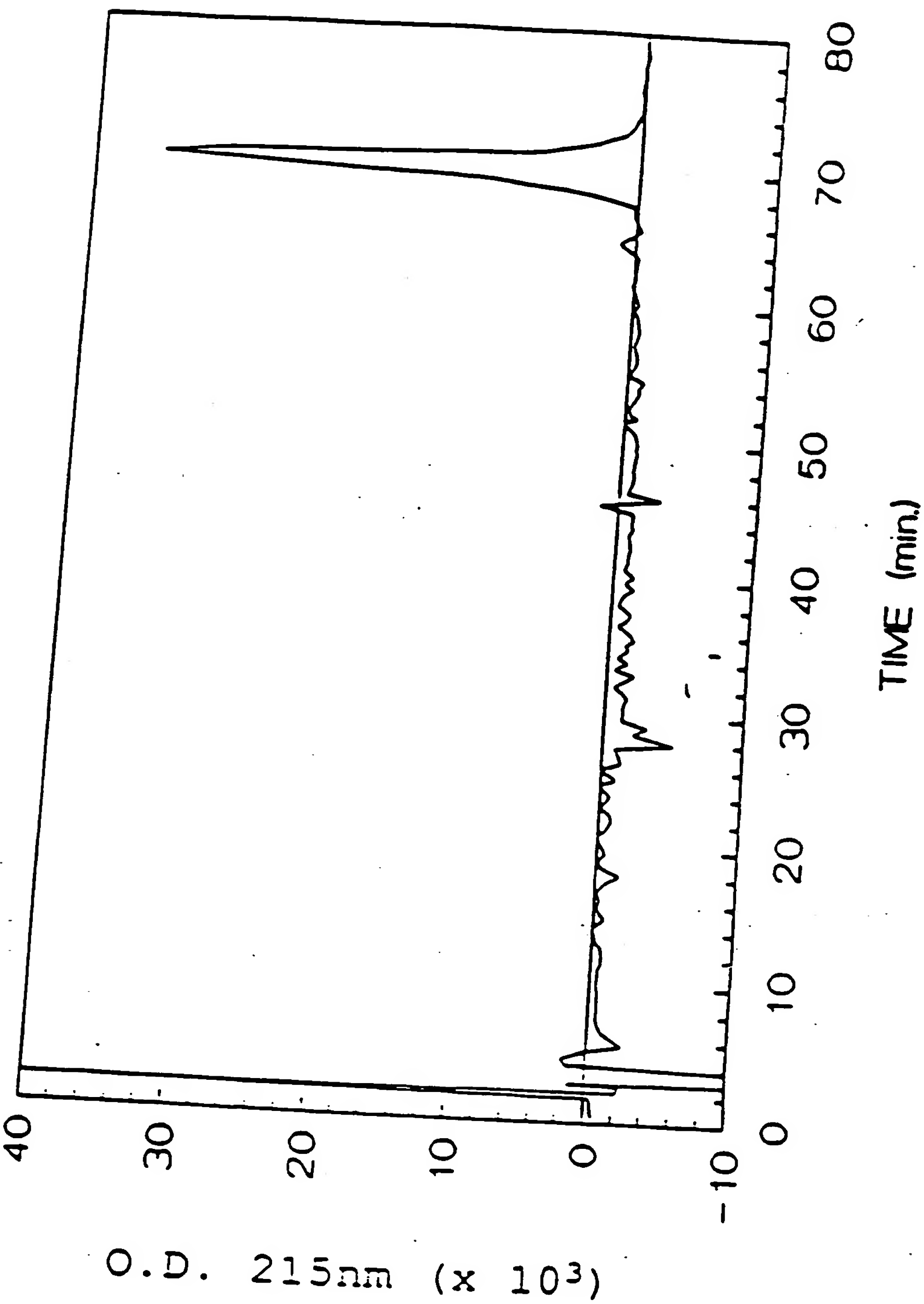


FIG.11

```
1                   10                     20
pE E I C R N P V T D N V K D I T K L V A N L P N D
 |---------------------------------------- Sequencing after
                                         |-------- T-5a -------
        30                   40                       50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment ------------->
                                              |----------------
----------------------------------- T-5a ---------------|
   |--------- CB-6a --------||------- CB-8; CB-10 ---------|
                      60                  70
H L S V S L T T L L D K F S N I S E G L S N Y S I
------ Sequencing after Trp Cleavage ---------------

        80                   90                       100
I D K L G K I V D D L V A C M E E N A P K N V K E
------------------------->
           |------------------ T-3 ------------------|       |---
                                                             |--
                                    |-CB-14;CB-15;CB-16 -
                                         |-------- S-1---------|
                      110                     120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----------------|---- T-4(N109 nonglyco) -----||-----------
----- T-7(N120 glyco);T-8(N109 nonglyco)-----|
------------------------- CB-14; CB-15; CB-16 -----------------
|----------------- S-5 or S-6 (N109 nonglyco)----------------
    130                  140                       150
F K D F M V A S D T S D C V L S S T L G P E K D S
---------------------------- T-5b ---------------------------------
------------------------------------------ CB-6B -------------------------
------ S-5 or S-6-----------                                       -
                      160
R V S V T K P F M L P P V A(A)
--||----- T-2 ---|                <-- <-- (Carboxypeptidase)
------ CB-6B ----------
----------------- S-2 ----------------------|
```

FIG.12A

```
OLIGO     SEQUENCE                          LOCATION

219-21    ACATTCTTIGGIGCATTCTCCTCCAT        393-368
            G  T        G  T  T

219-22    AAAAACTCCTCIGGIGTAAAATT           447-425
            G  T  T        G  G

219-25    GTTTCNGGTTTTTT                    420-407
            C     C  C

219-26    ATGGAAGAAAACGCCCCCAAAAACGT        368-393
               G  G  T        G  T

222-11    CCNAATGATTATATGATAAC              167-186
               C  C  C     C
                         T

222-12    GGNGGNAACATAAANGGCTT              566-585
                 G   G     T

223-6     ACCATAAAATCTTTAAAICGATC           492-470
              G  G  C  G     G

224-24    GTATTTTCAATAGATCCATTGA            450-471

224-25    CCAACTATGTCGCC                    190-202

224-27    GTAGTCAAGCTGACTGATAAG             273-253
```

FIG.12A CONT.'

224-28	TAACCAACAATGACTAGGCAA	235-215
225-31	TTCCAGAGTCAGTGTC	547-562
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35 *
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561 *
228-30	GATAAATGCAAGTGATAATCC	45-65
230-25	GCGGTCGACCCGCGGAACTTTAAGTCCATGCAACAC	705-685 *
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592 *
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595 *

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG. 12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG
	T
	A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

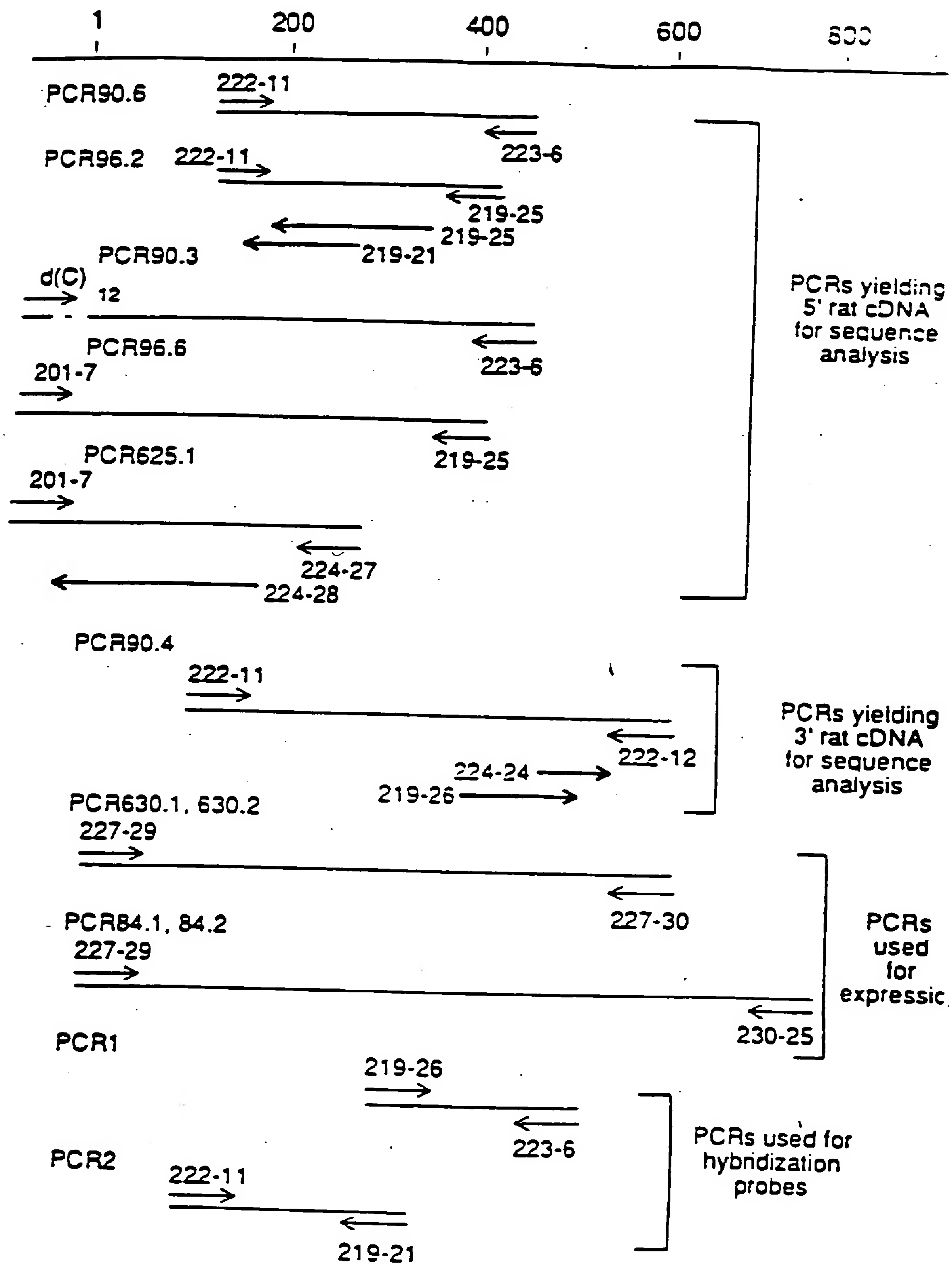
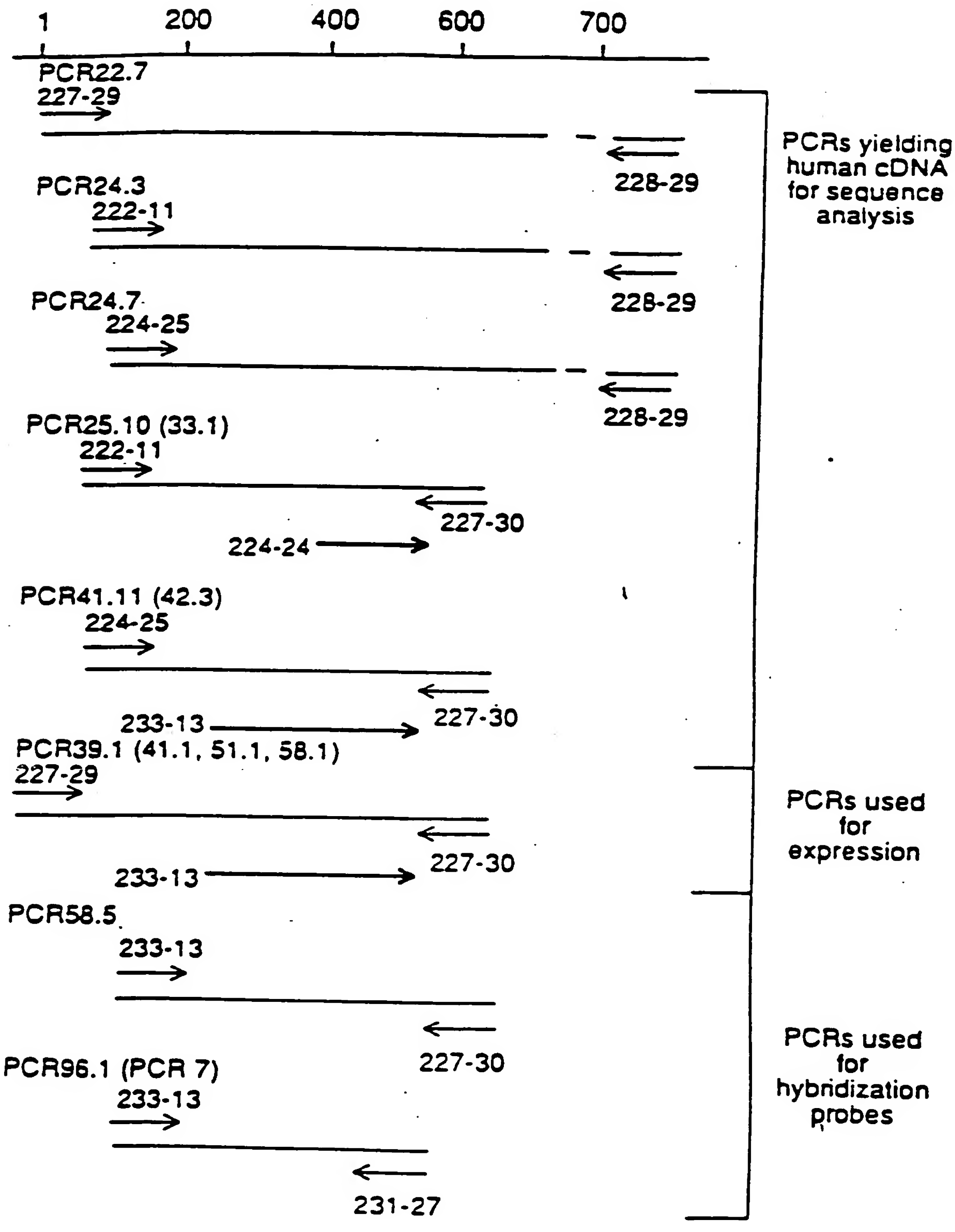

1
200
400
600
800
PCR90.6
222-11
223-6
PCR96.2
222-11
219-25
219-25
219-21
PCR90.3
d(C)
12
223-6
PCR96.6
201-7
219-25
PCR625.1
201-7
224-27
224-28
PCRs yielding 5' rat cDNA for sequence analysis
PCR90.4
222-11
222-12
224-24
219-26
PCRs yielding 3' rat cDNA for sequence analysis
PCR630.1, 630.2
227-29
227-30
PCR84.1, 84.2
227-29
230-25
PCRs used for expressic
PCR1
219-26
223-6
PCR2
222-11
219-21
PCRs used for hybridization probes

FIG.13B


1
200
400
600
700
PCR22.7
227-29
228-29
PCR24.3
222-11
228-29
PCR24.7
224-25
228-29
PCR25.10 (33.1)
222-11
227-30
224-24
PCR41.11 (42.3)
224-25
227-30
233-13
PCR39.1 (41.1, 51.1, 58.1)
227-29
227-30
233-13
PCR58.5
233-13
227-30
PCR96.1 (PCR 7)
233-13
231-27
PCRs yielding human cDNA for sequence analysis
PCRs used for expression
PCRs used for hybridization probes

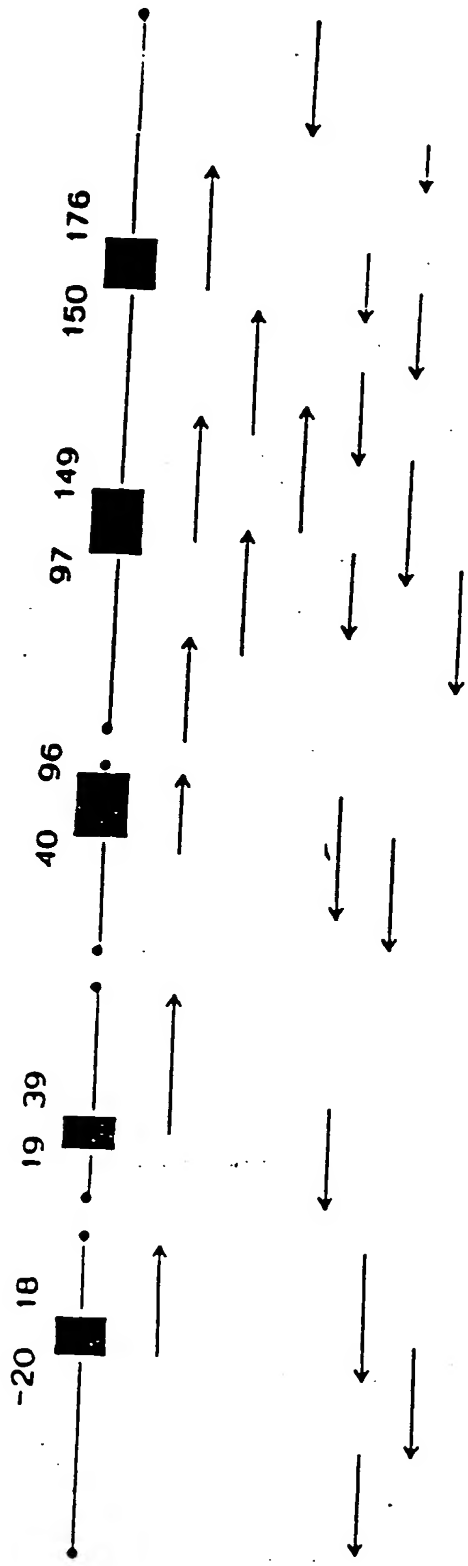


FIG.14A

FIG.14B

```
AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT    45
AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT    90
TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA   135
TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT   180
TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG   225
AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTCATGCATTCCT   270
CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG   315
CTACAAGTTCATCCCTAATTGCCGTCAAGAAACTGACTGTAGAAG   360
GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT   405
AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC   450
TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT   495
AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAAAAACCC   540
CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC   585
TGGTTTGCATAGTTCTGGATTTTTTTTTTTTTAAAAACTGATGGAC   630

                                  -20
                                  ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT   675

               -10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC   720

 1                        10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA   765

    18
hrLysLeu
```

FIG.14B CONT.'

```
CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC    810

CTGTGCTTGCTGACCACATAGGTTCAGGGCACTCCCGACAGGAGT    855

TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC    900

TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC    945

TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT    990

TTGCCTGTTACCTACTG                               1007

     Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA     45

TTTACAACTCAAGCATTATATATTGGACAACnACGGGTATGAGA     90

TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT    135

                                           19
                                          Val
TCTCTTGTATTTACTCACGTTTTCATTTCTTGGTCTCTGTAGGTG    180

                             30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC    225

          39
GlyMetAspValLeu
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT    270

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT    315

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT    360

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT    405

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA    450
```

FIG.14B CONT.'

```
CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG    495

TTAAAATCATGTTAAATTTCCTCCTTGGCTATGTTATTTCTCATG    540

GCTATGTTATTCCTATTCGTATTTCATTTAAAGGGACGGAATATT    585

TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA    630

TAAAA                                            635
```

Intervening sequence of unknown length

```
CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA    45

ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA    90

GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG    135

AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG    180

GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT    225

TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT    270

TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAAACTCTTTGTCCT    315

GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA    360

ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC    405

         40.                           50
     ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA    450

                      60
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT    495

      70                                80
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle
```

FIG.14B CONT.'

```
GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA     540

                              90                 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA     585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT                619

     Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA     45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA     90

ATATGTAGATACCACCTCTGCCACCTCAGCACATACATACACATA     135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC     180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT     225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT     270

AATTGTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG     315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC     360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC     405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT     450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC     495

AGTCAAGTCTATGAGTTATTTGAAAACTAGAATCTTTGTTAATTA     540

                                         97
                                  AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA     585

100                         110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu
```

FIG.14B CONT.'

```
GAATCACTGAAGAAGCCAGAAACTAGAAACTTTACTCCTGAAGAA     630

                120
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC     675

130                                  140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA     720

      148
GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT     765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC     810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA     855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT     900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA     945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT     990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA    1035

AGATTTCACGTCTCATGTCTTTTCCATAAGGTTCAAACTCTGAGA    1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC    1125

CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT    1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT    1215

TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC    1260

AGTTATGGTGTATCGCTTGACAAAACTGAGCAGCCAAGCTGAGTA    1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT    1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA    1395
```

FIG.14B CONT.

```
                                              150
                                           spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG    1440

                          160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT    1485

       170                 176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC    1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT    1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG    1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG    1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA    1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC    1755

GAAATTAATTGAAGGAAAAAAAAATACAAGCAAGGCCTTATTTTG    1800

AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT    1845

CAAAGTGGAGTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC    1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG    1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA    1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT    2025

TGcCCAAGAACCCAcGTTCCTGGAAGACTATCTTATTTTCATGTC    2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT    2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA    2160

AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA    2205
```

FIG.14B CONT.'

```
AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC    2250
CCTGAAAAATATATTTCACAGTGTAGACATTTGATATACATCTAA    2295
GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC    2340
CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC    2385
ATGCATATAACATATCAGATCCTCGAGC                     2413
```

FIG.14C

```
                              -25         -20
                               M  K  K  T  Q  T  W  I  I  T  C  I
CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT   60

      -10                 1
 Y  L  Q  L  L  L  F  N  P  L  V  K  T  Q  E  I  C  R  N  P
TTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC   120

       10                            20
 V  T  D  N  V  K  D  I  T  K  L  V  A  N  L  P  N  D  Y  M
TGTGACTGATAATGTAAAAGACATTACAAAACTGGTGGCGAATCTTCCAAATGACTATAT   180

       30                            40
 I  T  L  N  Y  V  A  G  M  D  V  L  P  S  H  C  W  L  R  D
GATAACCCTCAACTATGTCGCCGGGATGGATGTTTTGCCTAGTCATTGTTGGTTACGAGA   240

       50                            60
 M  V  T  H  L  S  V  S  L  T  T  L  L  D  K  F  S  N  I  S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC   300

       70                            80
 E  G  L  S  N  Y  S  I  I  D  K  L  G  K  I  V  D  D  L  V
TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT   360

       90                            100
 A  C  M  E  E  N  A  P  K  N  V  K  E  S  L  K  K  P  E  T
GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC   420

       110                           120
 R  N  F  T  P  E  E  F  F  S  I  F  N  R  S  I  D  A  F  K
TAGAAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA   480
```

FIG.14C CONT.'

```
130                                140
 D  F  M  V  A  S  D  T  S  D  C  V  L  S  S  T  L  G  P  E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA   540

150                                160
 K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S
GAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTTC   600

170                                180
 L  R  N  D  S  S  S  S  N  R  K  A  A  K  S  P  E  D  P  G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAAGTCCCCTGAAGACCCAGG   660

190                                200
 L  Q  W  T  A  M  A  L  P  A  L  I  S  L  V  I  G  F  A  F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTCGCTTGTAATTGGCTTTGCTTT   720

210                                220
 G  A  L  Y  W  K  K  K  Q  S  S  L  T  R  A  V  E  N  I  Q
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA   780

230                                240
 I  N  E  E  D  N  E  I  S  M  L  Q  Q  K  E  R  E  F  Q  E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA   840

248
 V
GGTGTAATT                                                      849
```

FIG.15A

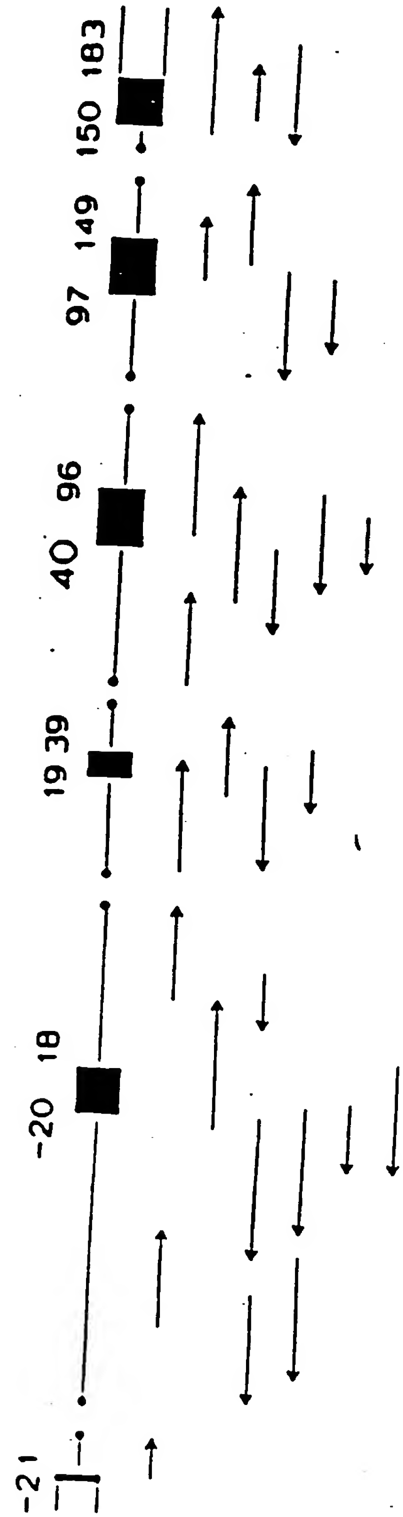


FIG.15B

-21
h:Gln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45
AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGACT 90
TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45
CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90
ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135
TGTTCGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180
TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225
GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT 270
TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315
TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360
GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405
ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450
CTCTAGTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495
TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540
AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585
CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630
AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B CONT.'

```
ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT     720

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC     765

                -20                            -10
                ThrTrpIleLeuThrCysIleTyrLeuGlnLe
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT     810

                                    1
uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs
GCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAA     855

         10                     18
nArgValThrAsnAsnValLysAspValThrLysLeu
TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA     900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT     945

CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT     990

AATGTTTTCCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA    1035

GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA    1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT    1125

TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT    1170

TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC    1215

CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA    1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT    1305

GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC    1350

ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT    1395

CATTGCCCACATGTTGAAGGACTCATCTCCCTGGTTTGTCACAT    1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC          1479
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC    45

CAAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA    90

GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT   135

TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT   180

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG   225

TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA   270

                                           19
                                       ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTGTCTCTGTAGGTGGCAA   315

                            30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA   360

          39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT   405

AGCTCATAGAAGAAATGGGATCATTCATATTGAGATAGTACACTA   450

GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA   495

TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT   535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCT    45

CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC    90
```

FIG.15B CONT.'

```
CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT    135

CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG    180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG    225

CCTGGCCAACATGGTGAAACTTCCTCTCTACTAAAAATAAAAAAG    270

TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA    315

GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG    360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT    405

                                 40
                                ProSerHisCysTrpIleS
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA    450

            50                                60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG    495

                                 70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

            80                                90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA    585

               96
ysGluAsnSerSerLys
AAGAAAACTCATCTAAGGTAACTTTGTGTTCATTGGGATTATTTT    630

TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG    675

AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTG    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG    765

CAGTTATACTGCAATACTGAAGTGCACATTC    796
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA    45

CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT    90

CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA   135

GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                         97
                                        AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA   225

                          110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT   270

              120                             130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG   315

                                    140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA   360

       148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA   405

AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG   450

TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG   495

CAGATATCAATAGCACAGAAGAAA                        519
```

Intervening sequence of unknown length

FIG.15B CONT.'

```
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG    45

                   150                                 160
                 spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT    90

                                 170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA    135

  176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT    225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA    270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG    315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT            352
```

FIG.15C

```
                 -25          -20
                  M  K  K  T  Q  T  W  I  L  T  C  I  Y  L  Q
AAGCTTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTTATCTTCAG   61

-10                          1                             10
 L  L  L  F  N  P  L  V  K  T  E  G  I  C  R  N  R  V  T  N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT   121

                            20                            30
 N  V  K  D  V  T  K  L  V  A  N  L  P  K  D  Y  M  I  T  L
AATGTAAAAGACGTCACTAAATTGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTC   181

                            40                            50
 K  Y  V  P  G  M  D  V  L  P  S  H  C  W  I  S  E  M  V  V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA   241

                            60                            70
 Q  L  S  D  S  L  T  D  L  L  D  K  F  S  N  I  S  E  G  L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTG   301

                            80                            90
 S  N  Y  S  I  I  D  K  L  V  N  I  V  D  D  L  V  E  C  V
AGTAATTATTCCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG   361

                           100                           110
 K  E  N  S  S  K  D  L  K  K  S  F  K  S  P  E  P  R  L  F
AAAGAAAACTCATCTAAGGATCTAAAAAAATCATTCAAGAGCCCAGAACCCAGGCTCTTT   421
```

FIG.15C CONT.'

```
                                    120                                 130
 T  P  E  E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V
ACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTGTA      401

                                    140                                 150
 V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E  K  D  S
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAGTCCTGAGAAAGATTCC      541

                                    160                                 170
 R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S  L  R  N
AGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGAAT      601

                                    180       183
 D  S  S  S  S  N  S  K  Y  I  Y  L  I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT      661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATTGA      721

TACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAATTA      781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG                           820
```

FIG. 15D

```
GAGCTCCGAGCcCTCtCTGGCGCgCgAGGTATTTCGTCTGTnCCCGGGGGTGCCAGGTGA    60
GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC   120
AAGCTTCGCCCTCTGCGTCCCCGCGCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC   180
CCCAGGCGAGCGGACAAGGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC   240
TGGCCGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCCGGGCTC   300
CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGCGGGCGGGAACTGTATAAAAGCGCCGGCGG   360
CTCAGCAGCCGGCTTCGCTCGCCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG   420
GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGT   480
TCGTGCAAT[illegible]TGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC   540

                              -25           -21
                              MetLysLysThrGln
TGGATCGG[illegible]TGCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGCGCCCGGGA   600
GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCCGGGGAAGCCGGCGCTCCCTGG   660
GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA   720
GGCCGGCGTGGTGTGTGATCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA   780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG   840
TCGGAAACCGTAATTCCCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT   900
ATCAC                                                           905
```

FIG. 15D CONT.

```
             Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA   60

AAATAAGTCATGCATAAAAGCAACTATAATACATAATAGAAAATGTTATTTTCAAGCCGA  120

TGTGTAGGTTATGTGTGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT  180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT  240

TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAATTCTCTTAGGTCTAAAAATAT  300

ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA  360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAATAAGATGTTTCTTT  420

TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCTAAGGGCT  480

AAGTCTTTAACATGCTGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA  540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATTCAAAATGGATTTTAA  600

CTAAAAGCTTTTAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT  660

AAGCCAATAACATATATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT  720

                                                          -20
                                                           Th
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTCTGTTTTCATTTAGAC  780

                        -10
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGl
TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA  840
```

FIG. 15D CONT.

```
1                                      10                                     18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA   900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTTGAT   960

AAAAGATTTAGATTTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGGAAAGTAATCA   1020

CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA   1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGGTCTTC   1140

TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG   1200

CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA   1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC   1320

CCAATTCAATGAGCAGGAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA   1380

CATAGAGAGGTGATTCATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT   1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC                         1479
```

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT   60

TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTTTA   120

TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT   180
```

FIG. 15D CONT.

```
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTGTGTGCTTTTCTCCAA   240

AGCACTACAAATATGATTAATTGATGTATAAGAATTTTCTTATGGAATTTTTTTTTTTGT   300

     19
     ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA   360

     39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA   420

TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG   480

GATTTGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT        535

            Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTCACACTAGTC   60

CCTTCTCTTCCTGTTACAATAACCCCTGTCCTCCTATTACAACATTTTAAGTAATGTAAT   120

ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG   180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAACATGGT   240

GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACTTGTAAT   300

CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG   360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGTTTTGTCTCTTTTTTC   420
```

FIG. 15D CONT.

```
         40                                               50
         ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGCAGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT    480

         60                                               70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

         80                                               90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAAACTCATCTA    600
96
ys
AGGTAACTTTGTGTTCATTGGGATTATTTTTCATTACGCTTCTCTAAAAACCCATGCTTC    660

TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTGCAGTTATACTGCAAT    780

ACTGAAGTGCACATTC
                                                                796

                  Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCTGCATTACC    60

AATCTGAATTACATACGTTAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAAATA   120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA    180

                                     97
                                     AspLeuLysLysSerPheLysSerP
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAAAATCATTCAAGAGCC    240
```

FIG. 15D CONT.

```
                    110                                               120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATG    300

                    130                                               140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA    360

            148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAAACTTAAA    420

TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTTAAGCTGTAGCAAGATACATGCATGTA    480

CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAAACTAATGATTGTAGATTTGTGGG   541


                 Intervening sequence of unknown length


                                                              spS
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTGCTTTCTATTTAGATT    60

150                           160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
CCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGA    120

170            176
snAspSerSerSerSerAsnA
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT    240

GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT    300
```

FIG. 15D CONT.

```
TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTTCTGCTGA    360
GGTTATTTTAAATAAGACATAAAATTAATTTTAGAAATATGATTTATGCCTTTTGTTGAA    420
TCATTAACATATAT
                                                                 434
```

Intervening sequence of unknown length

```
ACAGAAACAGTTAAAACAACCACAGCATAAGAGnAAAACTTCTAGAATGGATATGCTGTA    60
                         178
                    rgLysAlaLysAsnProProGlyAspSerSerL
TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC    120
   190                             200
euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGCCAGCCATGGCATTGCCAGCATTGTTTTCTCTTATAATTGGCTTTGCTTTTG    180
                 213
lyAlaLeuTyrTrpLys
GAGCCTTATACTGGAAGGTAAGTGGTACCATTCCTTtTTTTAAAAATATGCTATGTtTAC    240
ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAACAGTGAATCTACCT    300
TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGTCTGGA    360
GACAATCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT
                                                                404
```

Intervening sequence of unknown length

FIG. 15D CONT.

```
AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA   60
                                                       214
                                                       LysArgG
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC   120
        220                                  230       235
lnProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS
AGCCAAGTCTTACAAGGCCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA   180
e
GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG   240

TGTACCTGCCCATAATGTCTTTAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT   300

GAGTCCCAACTCTATCCATGTTTCTGATGTCTCACTCTCTCTTC                   344

                 Intervening sequence of unknown length

GTATGTGTATATGCATATACAGAGAAAGAAATGTTTTAACTACTTGGAAAGACTACCTTA   60

AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAAGGTAGGCTCCCCCATTCAAT   120

TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG   180

                                                          rM
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTCAGTA   240
237                                  248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTGCAAGAGaAAGAGAGAGAGTTTCAAGAAGTGTAATTGTGGCTTGTATCAACACTGT   300

TACTTTCGTACATTGGTAAGTTTTTTTCTTCTTTCCTTTTTTTTTCTTTTTTTTATTATA   360
```

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTTACGTATGTTTACATGTGC 420

CATGTT 426

FIG.16A

	-25				25
Human	MKKTQTWILT	CIYLQLLLFN	PLVKTEGICR	NRVTNNVKDV	TKLVANLPKD
Monkey	MKKTQTWILT	CIYLQLLLFN	PLVKTEGICR	NRVTNNVKDV	TKLVANLPKD
Dog	MKKTQTWIIT	CIYLQLLLFN	PLVKTKGICG	KRVTDDVKDV	TKLVANLPRD
Cat	MKXTQTWIVT	CIYLQXLLFN	PLVKTKGLCR	NRVTDDVKDV	TKLVANLPRD
Cow	MKKTQTWIIT	CIYLQLLLFN	PLVHTQGICS	NRVTDDVKDV	TKLVANLPRD
Rat	MKKTQTWIIT	CIYLQLLLFN	PLVKTQEICR	NPVTDNVKDI	TKLVANLPND
Mouse	MKKTQTWIIT	CIYLQLLLFN	PLVKTKEICG	NPVTDNVKDI	TKLVANLPND
Chicken	TWIIT	CFCLQLLLLN	PLVKAQSSCG	NPVTDDVNDI	ARLVGNLPND
Scfpep	MKkTQTWIiT	CiyLQlLLfN	PLVkt.giCr	nrVTd.VkDv	tKLVaNLPkD

	26				72
Human	YMITLKYVPG	MDVLPSHCWI	SEMVVQLSDS	LTDLLDKFSN	ISEG...LSN
Monkey	YMITLKYVPG	MDVLPSHCWI	SEMVVQLSDS	LTDLLDKFSN	ISEG...LSN
Dog	YKIALKYVPG	MDVLPSHCWI	SVMVEQLSVS	LTDLLDKFSN	ISEG...LSN
Cat	YKIALKYVPG	MDVLPSHCWI	SVMVEQLSVS	LTDLLDKFSN	ISEG...LSN
Cow	YMITLKYVPG	MDVLPSHCWI	SEMVEQLSVS	LTDLLDKFSN	ISEG...LSN
Rat	YMITLNYVAG	MDVLPSHCWL	RDMVTHLSVS	LTTLLDKFSN	ISEG...LSN
Mouse	YMITLNYVAG	MDVLPSHCWL	RDMVIQLSLS	LTTLLDKFSN	ISEG...LSN
Chicken	YLITLKYVPK	MDSLPNHCWL	HLMVPEFSRS	LHNLLQKFSD	ISDMSDVLSN
Scfpep	YmItLkYVpg	MDvLPsHCWi	seMVeqlSvS	LtdLLdKFSn	ISeg...LSN

	73				121
Human	YSIIDKLVNI	VDDLVECVKE	NSSKD.LKKS	FKSPEPRLFT	PEEFFRIFNR
Monkey	YSIIDKLVNI	VDDLVECVKE	NSSKD.LKKS	FKSPEPRLFT	PEEFFRIFNR
Dog	YSIIDKLVKI	VDDLVECTEG	YSFEN.VKKA	PKSPELRLFT	PEEFFRIFNR
Cat	YSIIDKLVKI	VDDLVECVEG	HSSEN.VKKS	SKSPEPRLFT	PEEFFRIFNR
Cow	YCIIDKLVKI	VDDLVECMEX	HSSEN.VKKS	SKSPEPRQFT	PEKFFGIFNK
Rat	YSIIDKLGKI	VDDLVACMEE	NAPKN.VKES	LKRPETRNFT	PEEFFSIFNR
Mouse	YSIIDKLGKI	VDDLVLCMEE	NAPKN.IKES	PKRPETRSFT	PEEFFSIFNR
Chicken	YSIINNLTRI	INDLMACLAF	DKNKDFIKEN	GHLYEEDRFI	PENFFRLFNS
Scfpep	YsIIdkLvkI	vdDLveC.ee	nsskn.vKks	.kspEprlFt	PEeFFrIFNr

FIG.16B

```
        122                                                     169
Human   SIDAFKDF.V VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Monkey  SIDAFKDF.A VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Dog     SIDAFKDLET VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
Cat     SIDAFKDLEM VASKTSECVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Cow     SIDAFKDLEI VASKMSECVI SSTS.SPEKD SRVSVTKPFM LPPVAASSLR
Rat     SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Mouse   SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Chicken TIEVYKEFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
Scfpep  sIdafKdf.m vasktsdCvv sSTl.sPekD SRVsVTKpfm lPPVAASSLR

        170                                                     213
Human   NDSSSSNRKA KNPPGD.... ..SSLHWAAM ALPALFSLII GFAFGALYWK
Monkey  NDSSSSNRKA KNPTGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK
Dog     NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFAFGALYWK
Cat     NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPACFSLVI GFAFGAFYWK
Cow     NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFAFGAFYWK
Rat     NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFAFGALYWK
Mouse   NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFAFGALYWK
Chicken NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK
Scfpep  NDSssSNrka .n..ed.... ..sslqwaam ALpalfSLvI GFafGAlYWK

        214                                      248
Human   KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREFQEV
Monkey  KRQPSLTRAV ENIQIN...E DDNEISMLQE KEREFQEV
Dog     KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cat     KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cow     KKQPNLTRTV ENRQIN...E EDNEISMLQE KEREFQEV
Rat     KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Mouse   KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQQ KEREHLQV
Scfpep  Kkqpsltrav eniqin...e edNEISMLQe KErEfqeV
```

FIG. 16C

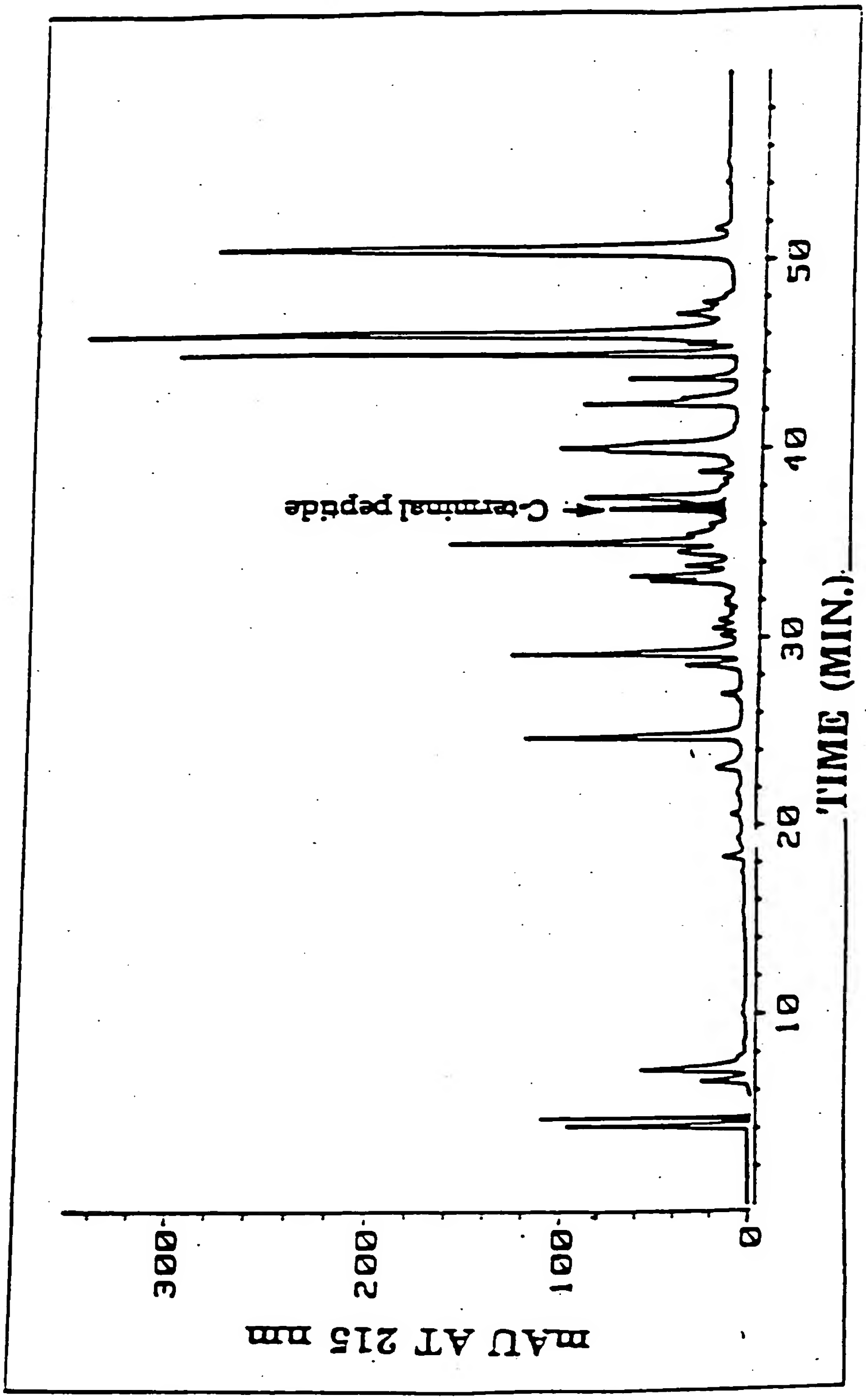

C-terminal peptide
TIME (MIN.)
mAU AT 215 nm
0
100
200
300
10
20
30
40
50

FIG. 16D

```
EcoRI
           ta  a   t   t   t a a      t   t   c      g      t   a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V

  g  a  t       ta gt   t  t  g      t  a   at a ag   t   g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E

                  BstEII
        t   a a   ca gt   c   a       a   t   t a   c   t   a
AAAGACTCCCGTGTTTCGGTTACCAAACCGTTCATGCTGCCGCCGGTTGCT
K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A

 c ag        t a g   t    ag  ag t ag  ag t   tag t   g     a  t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACTCCAAATACATCTAC
A  S  S  L  R  N  D  S  S  S  S  N  S  K  Y  I  Y

             BamHI
    t
CTGATCTAATAGGATCC
L  I  •  •
```

FIG. 16E

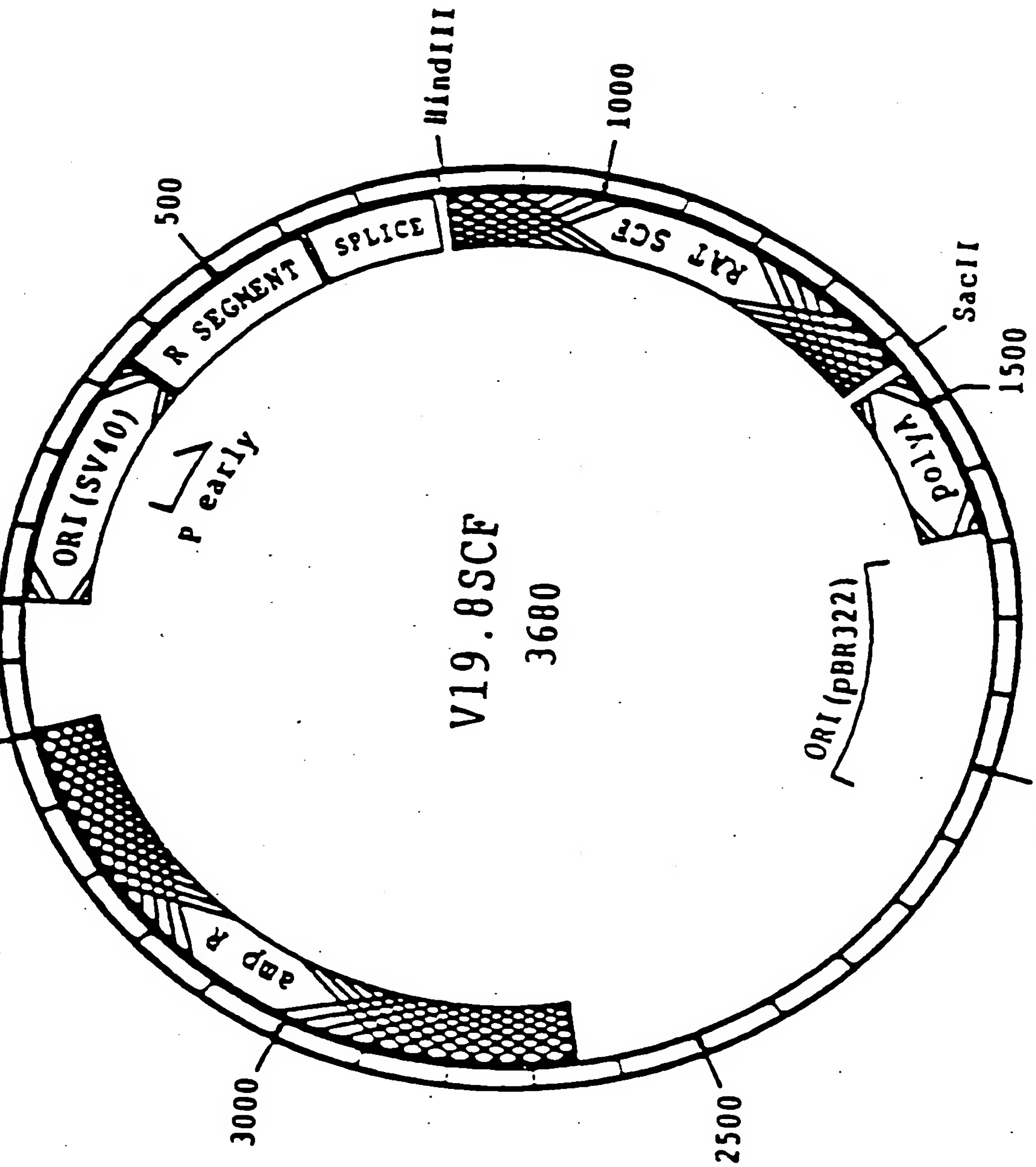
BstEII

BamHI

GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC

V T K P F M L P P V A A • •

FIG.17


HindIII
1000
500
SPLICE
RAT SCF
R SEGMENT
SacII
1500
ORI (SV40)
P early
polyA
3680
V19.8SCF
3680
ORI (pBR322)
3500
2000
amp R
3000
2500

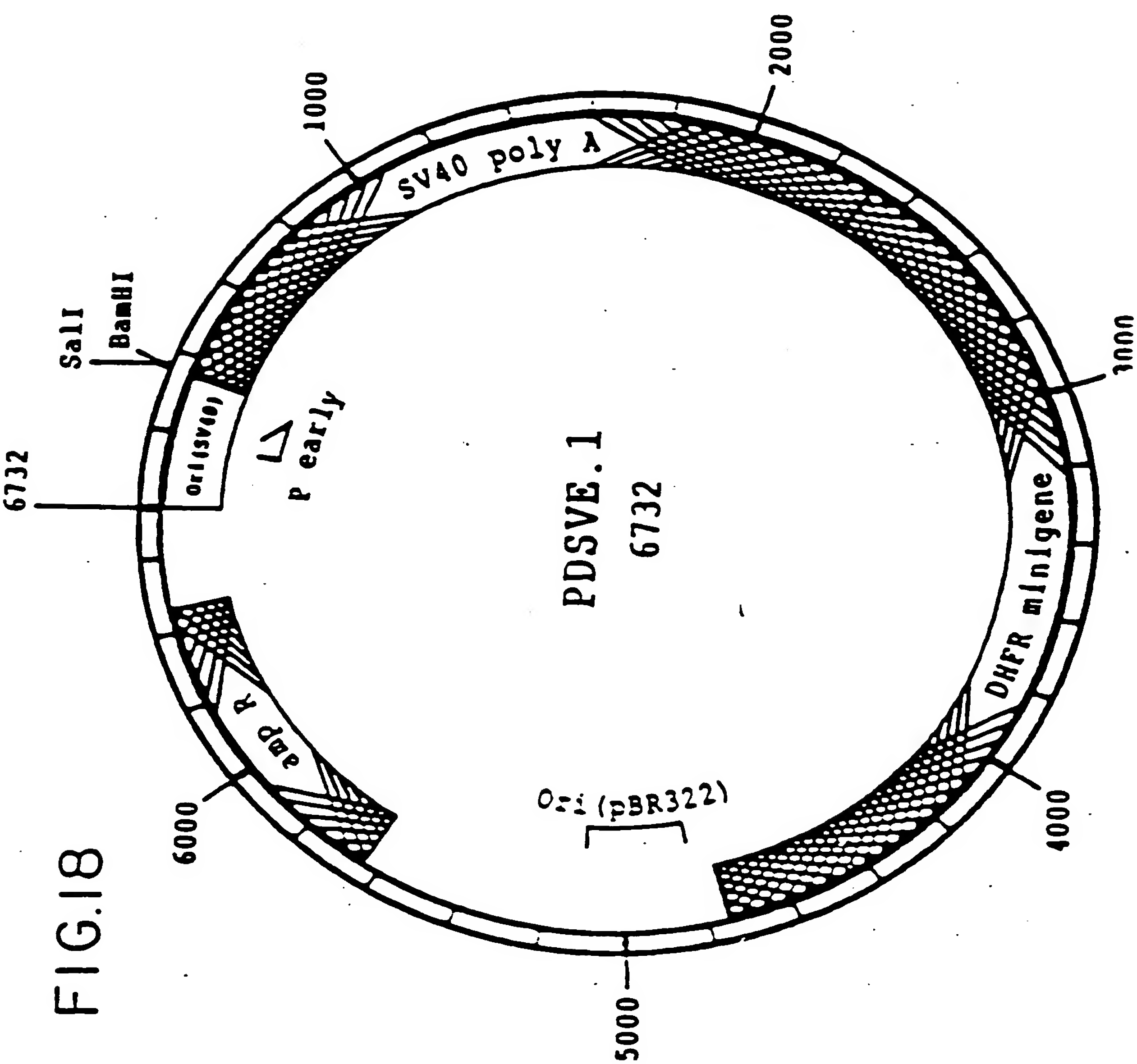

PDSVE.1
6732
SV40 poly A
DHFR minigene
amp R
Ori (pBR322)
Ori (SV40)
P early
SalI
BamHI
6732
1000
2000
3000
4000
5000
6000

FIG.18

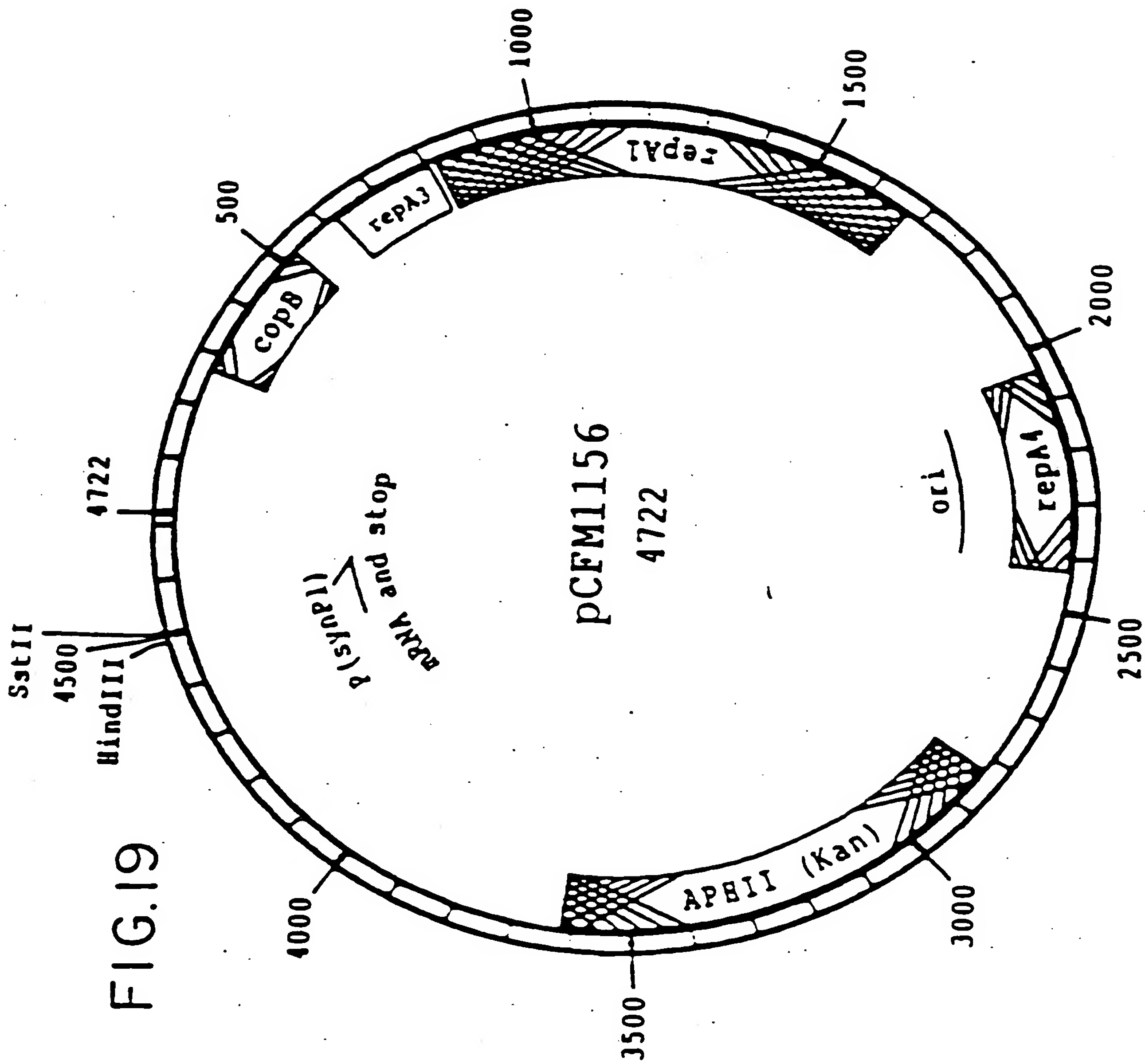

pCFM1156
4722
repA1
repA3
copB
repA4
ori
APHII (Kan)
p(synPl)
mRNA and stop
SstII
4500
HindIII
4722
500
1000
1500
2000
2500
3000
3500
4000

FIG.19

FIG.20A

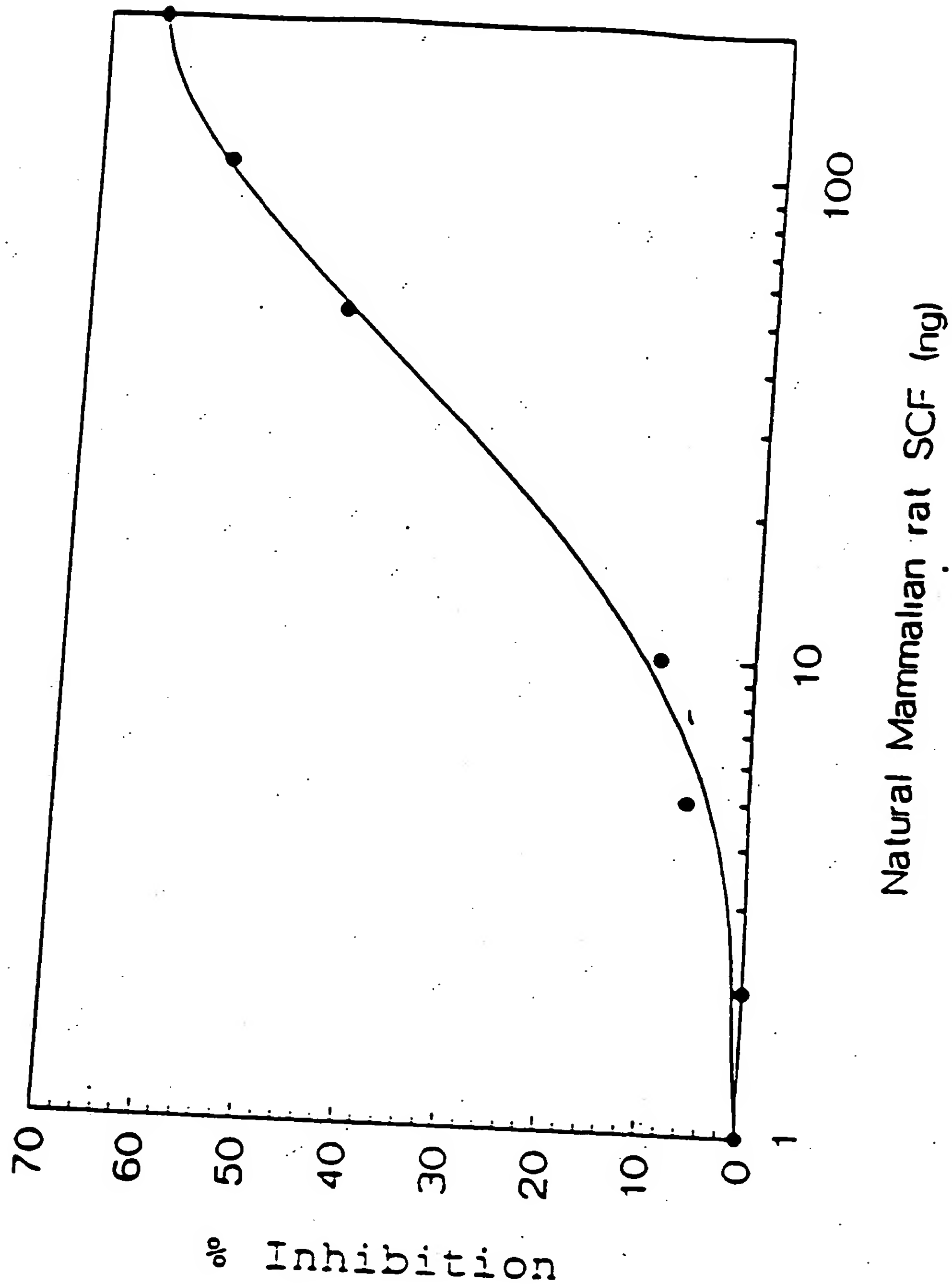

% Inhibition
0
10
20
30
40
50
60
70
Natural Mammalian rat SCF (ng)
1
10
100

FIG. 20B

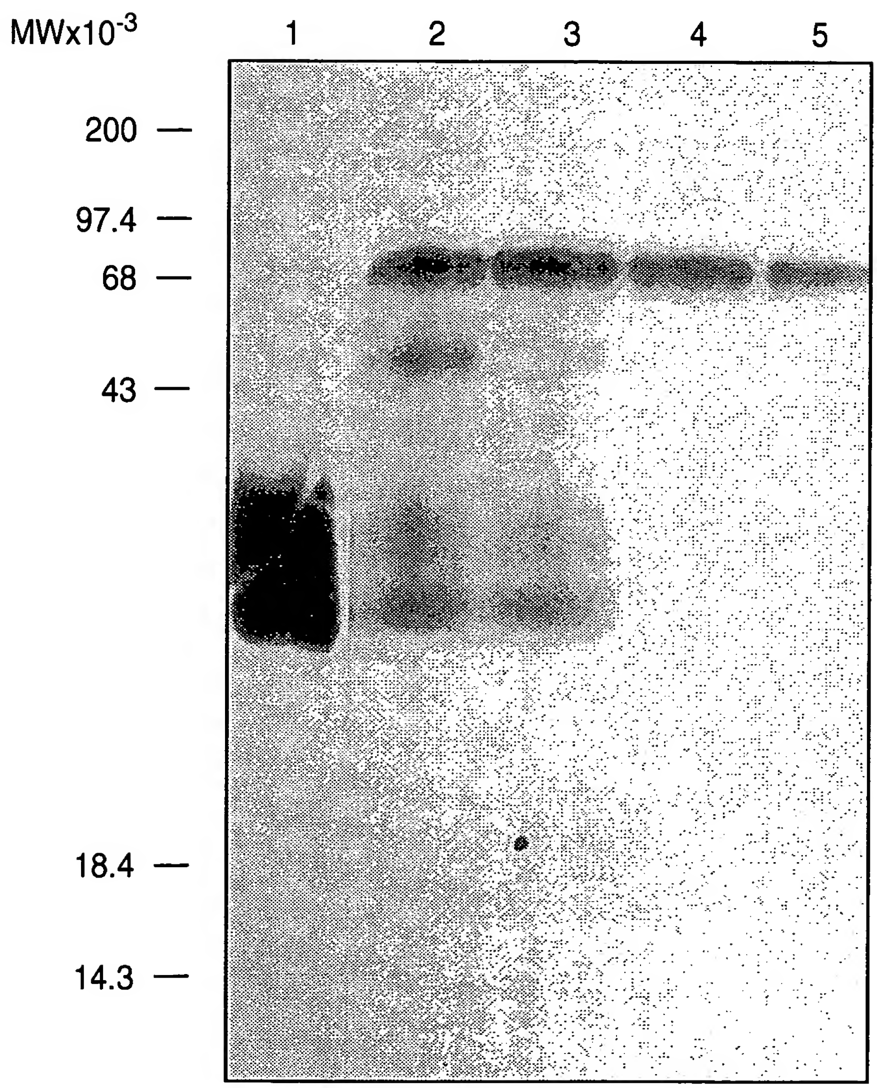


FIG. 21

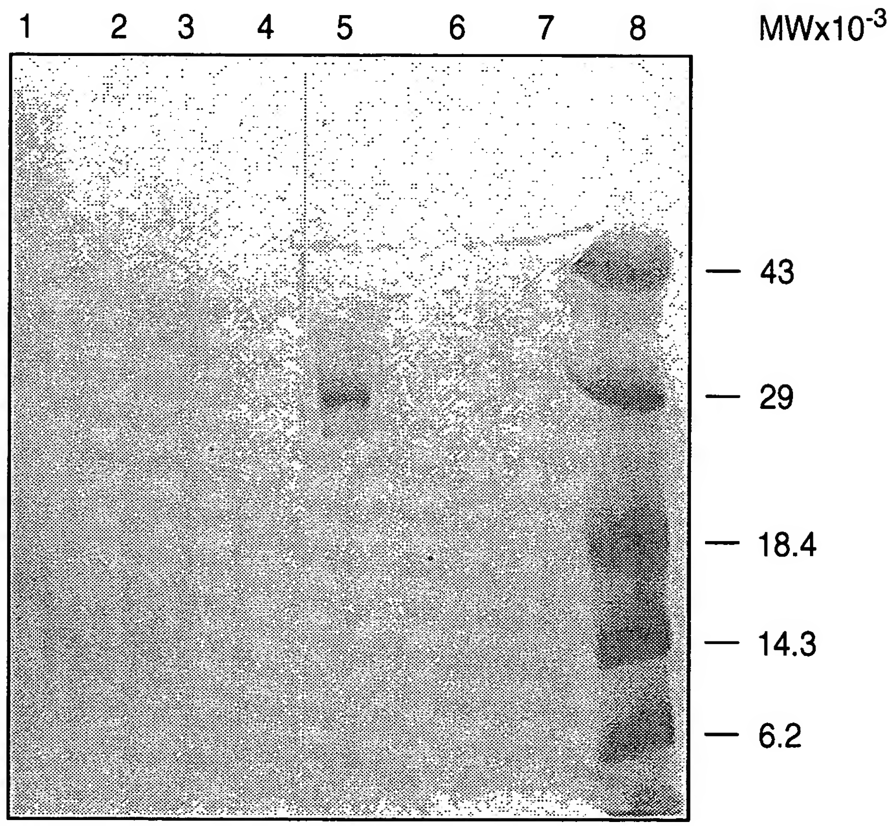


FIG. 22

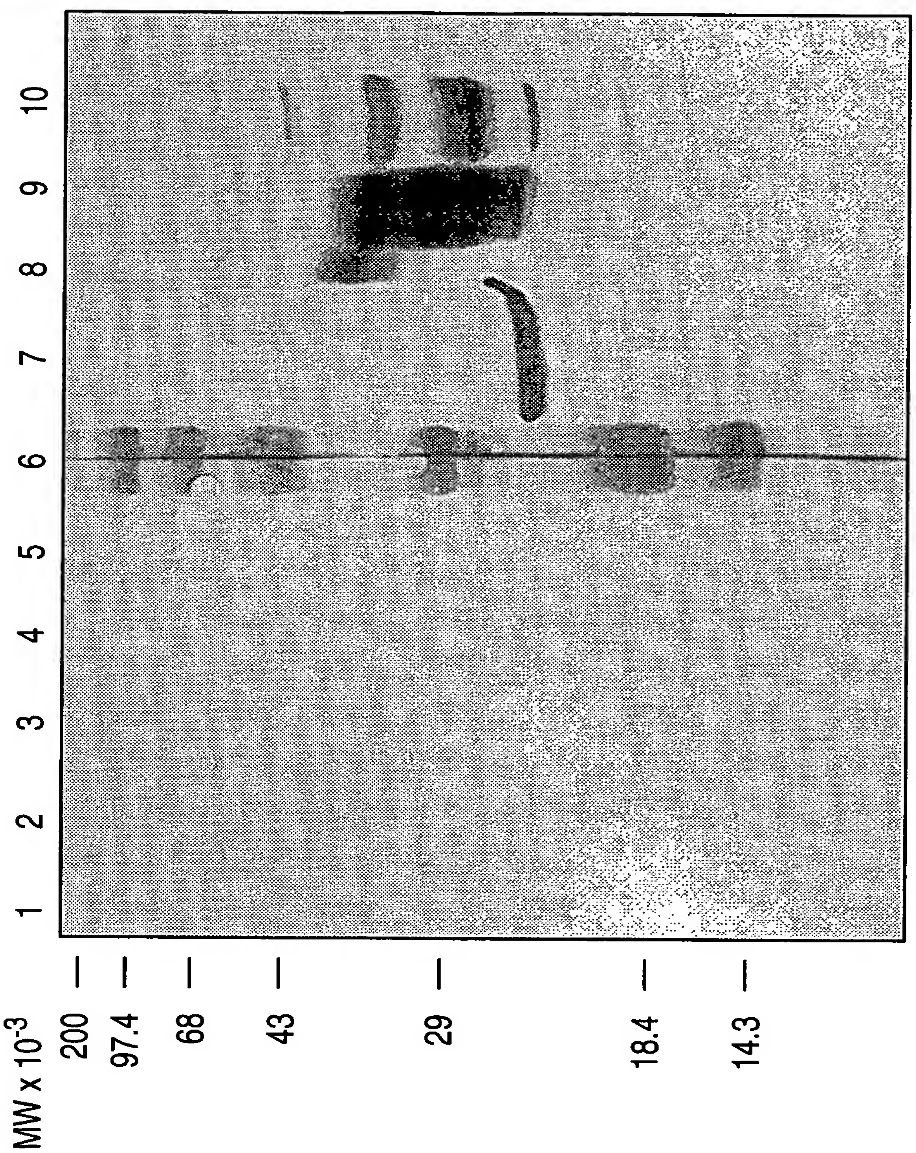


FIG. 22A

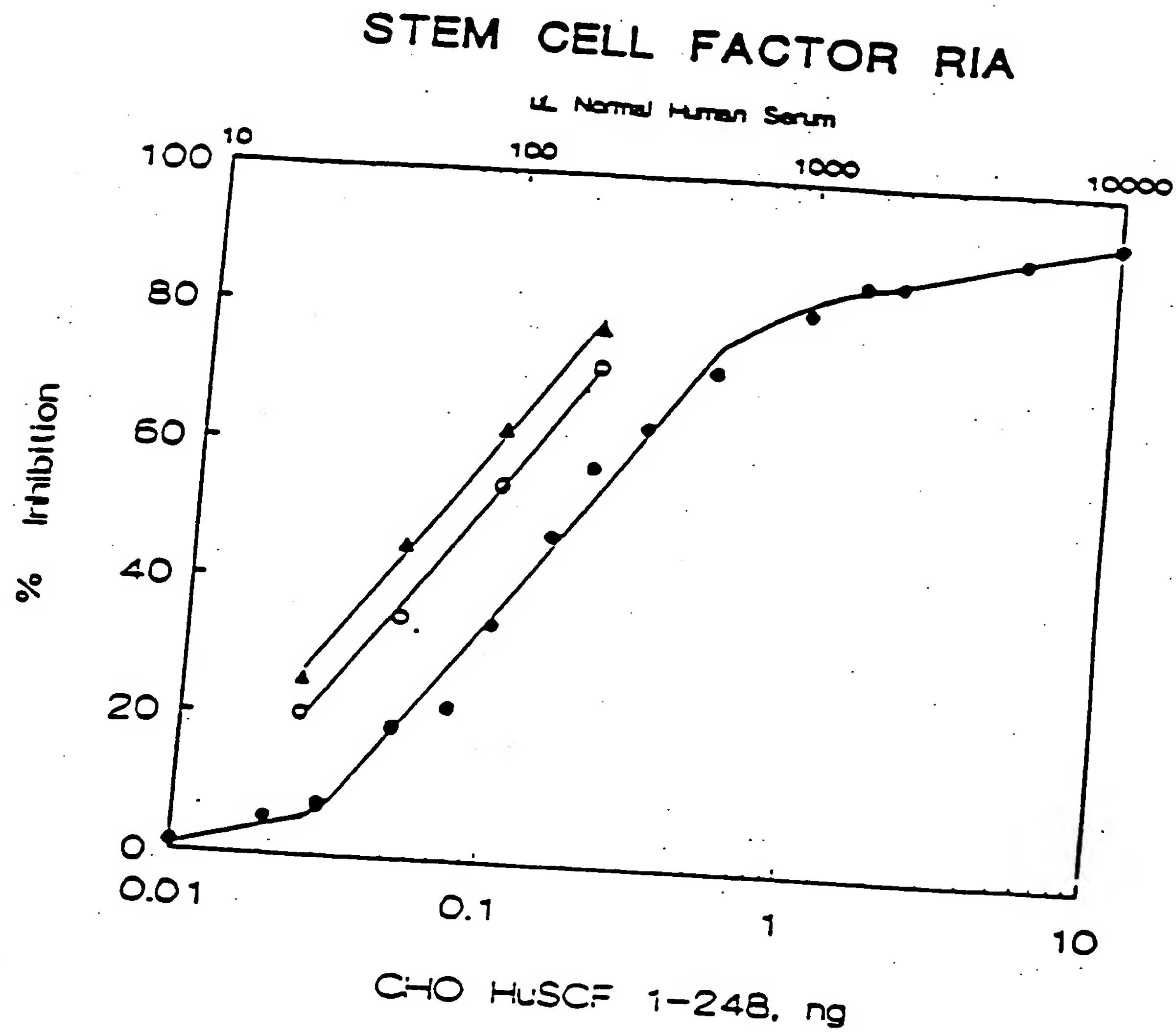

STEM CELL FACTOR RIA
uL Normal Human Serum
10
100
1000
10000
100
80
60
40
20
0
% Inhibition
0.01
0.1
1
10
CHO HuSCF 1-248, ng

FIG. 23

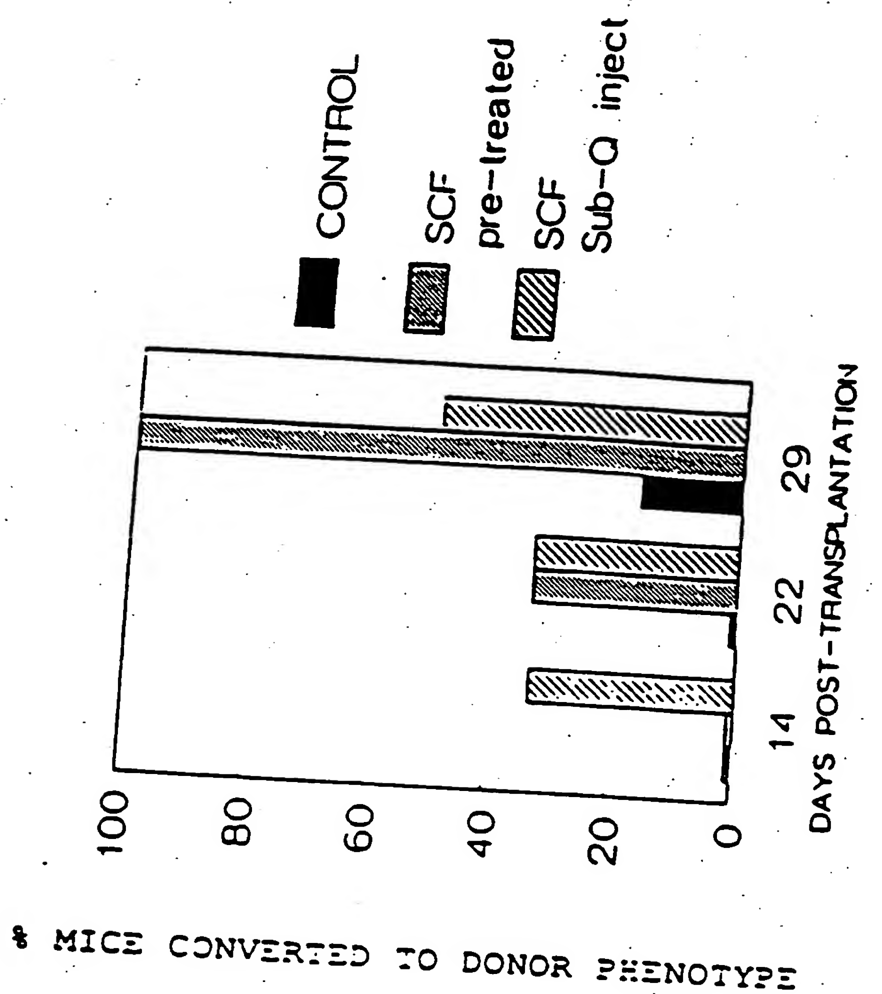

CONTROL
SCF pre-treated
SCF Sub-Q inject
100
80
60
40
20
0
14
22
29
DAYS POST-TRANSPLANTATION
% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

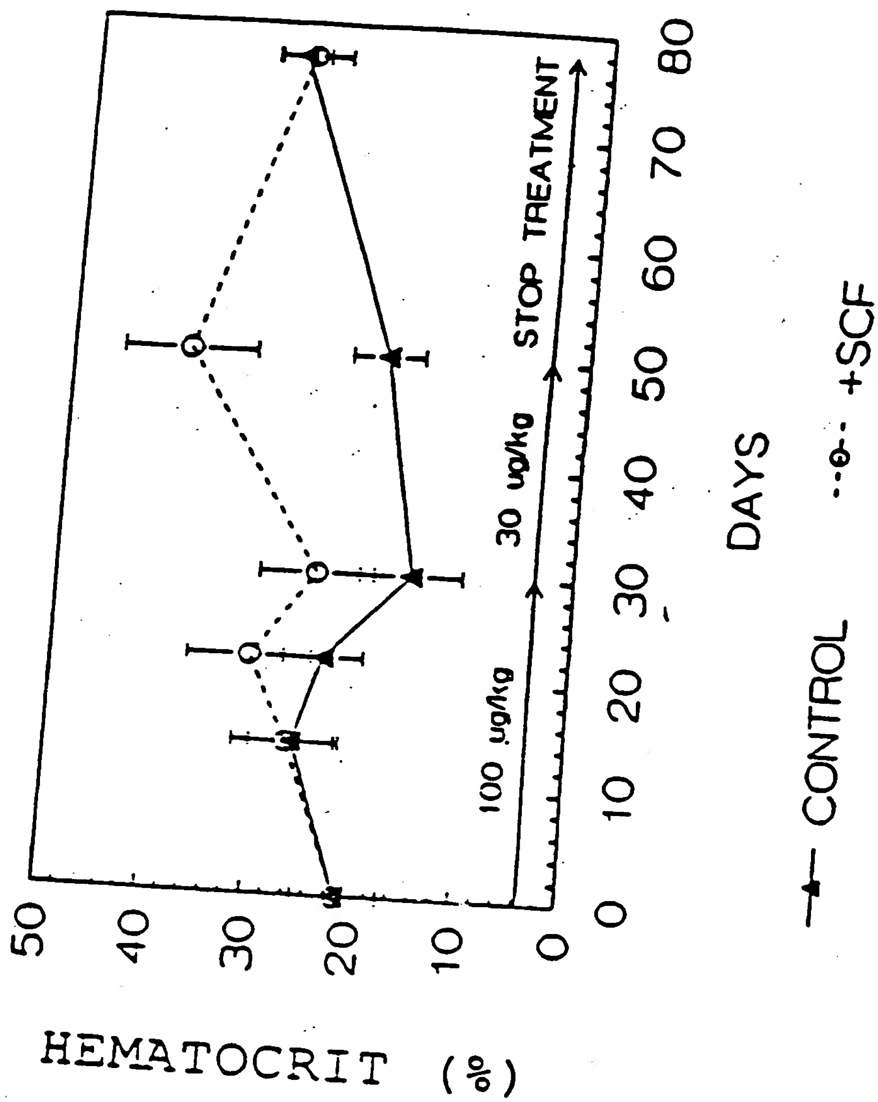

HEMATOCRIT (%)
0
10
20
30
40
50
DAYS
0
10
20
30
40
50
60
70
80
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 24B

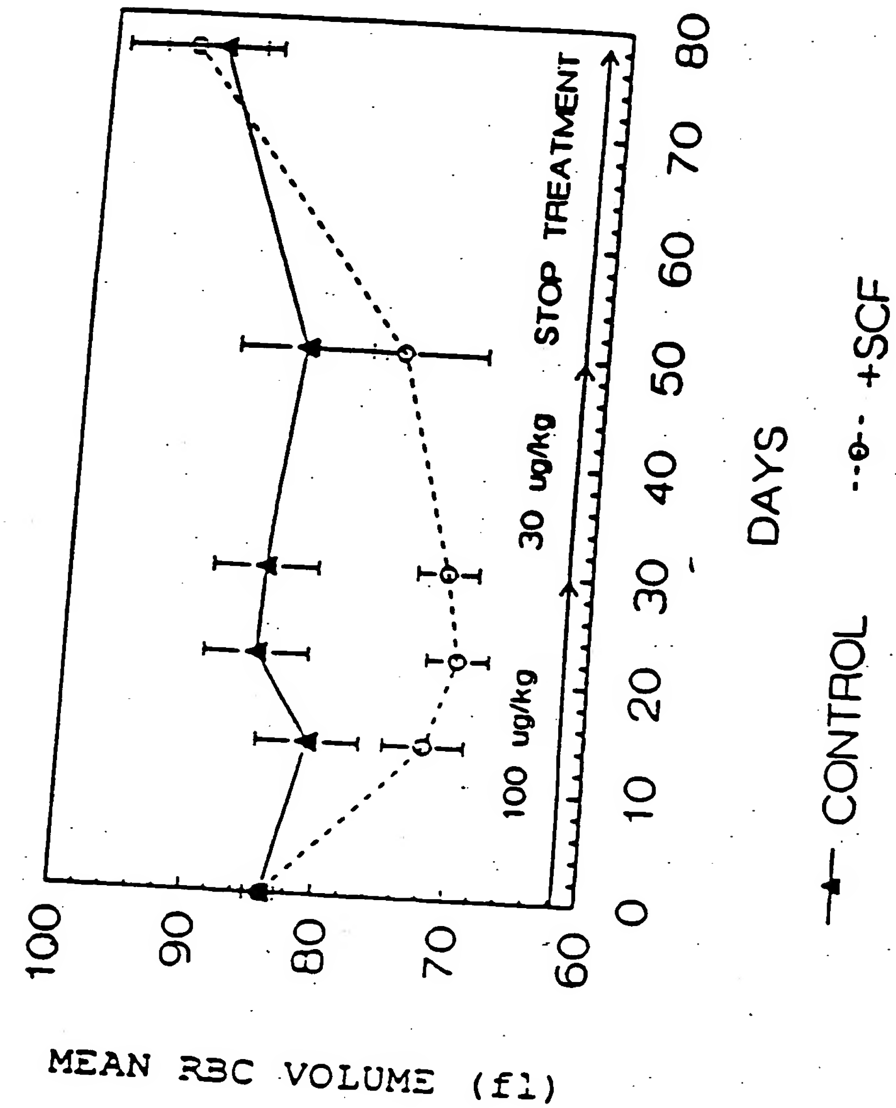

MEAN RBC VOLUME (fl)
100
90
80
70
60
0
10
20
30
40
50
60
70
80
DAYS
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 25

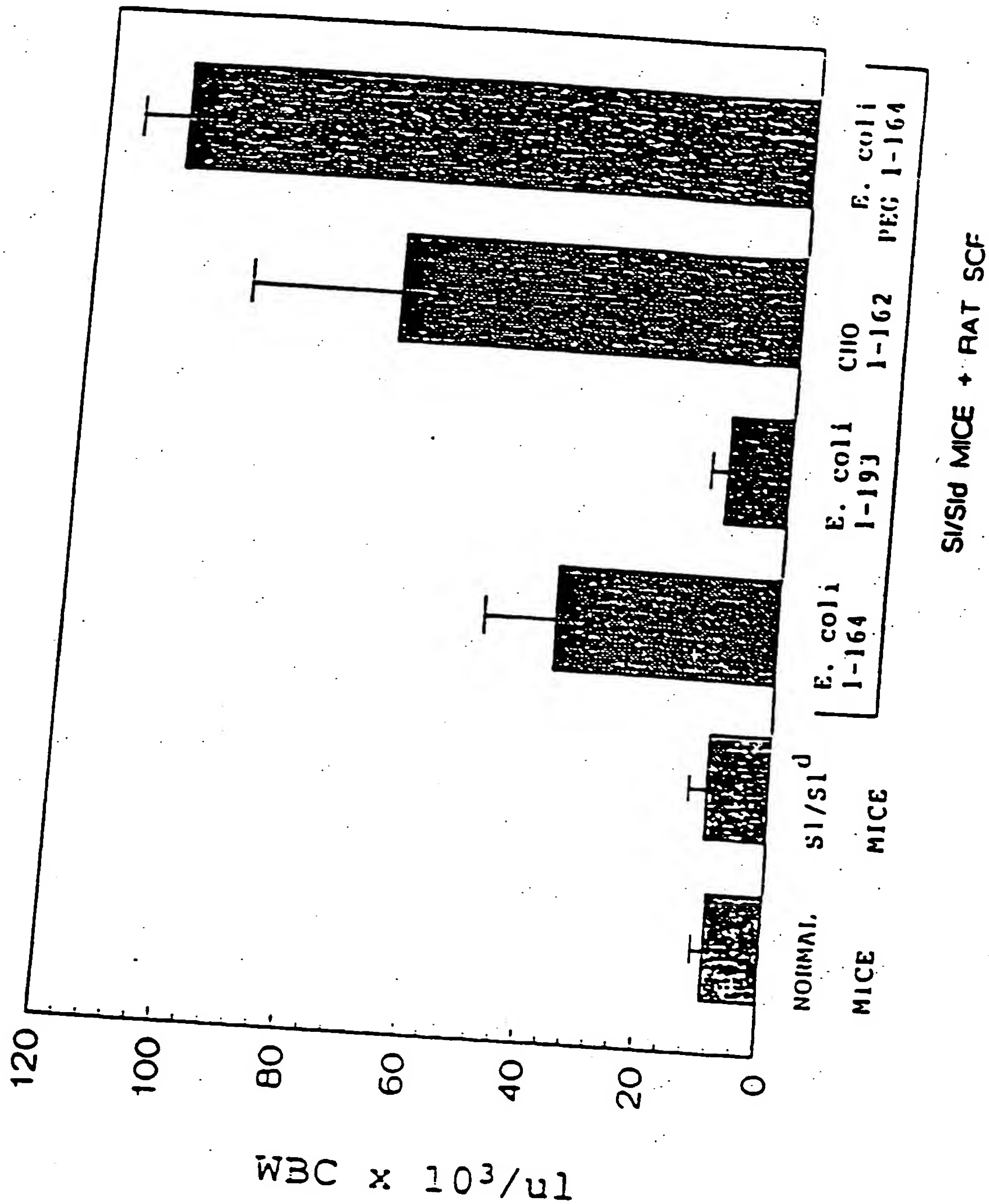

WBC x 10³/ul
0
20
40
60
80
100
120
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 26

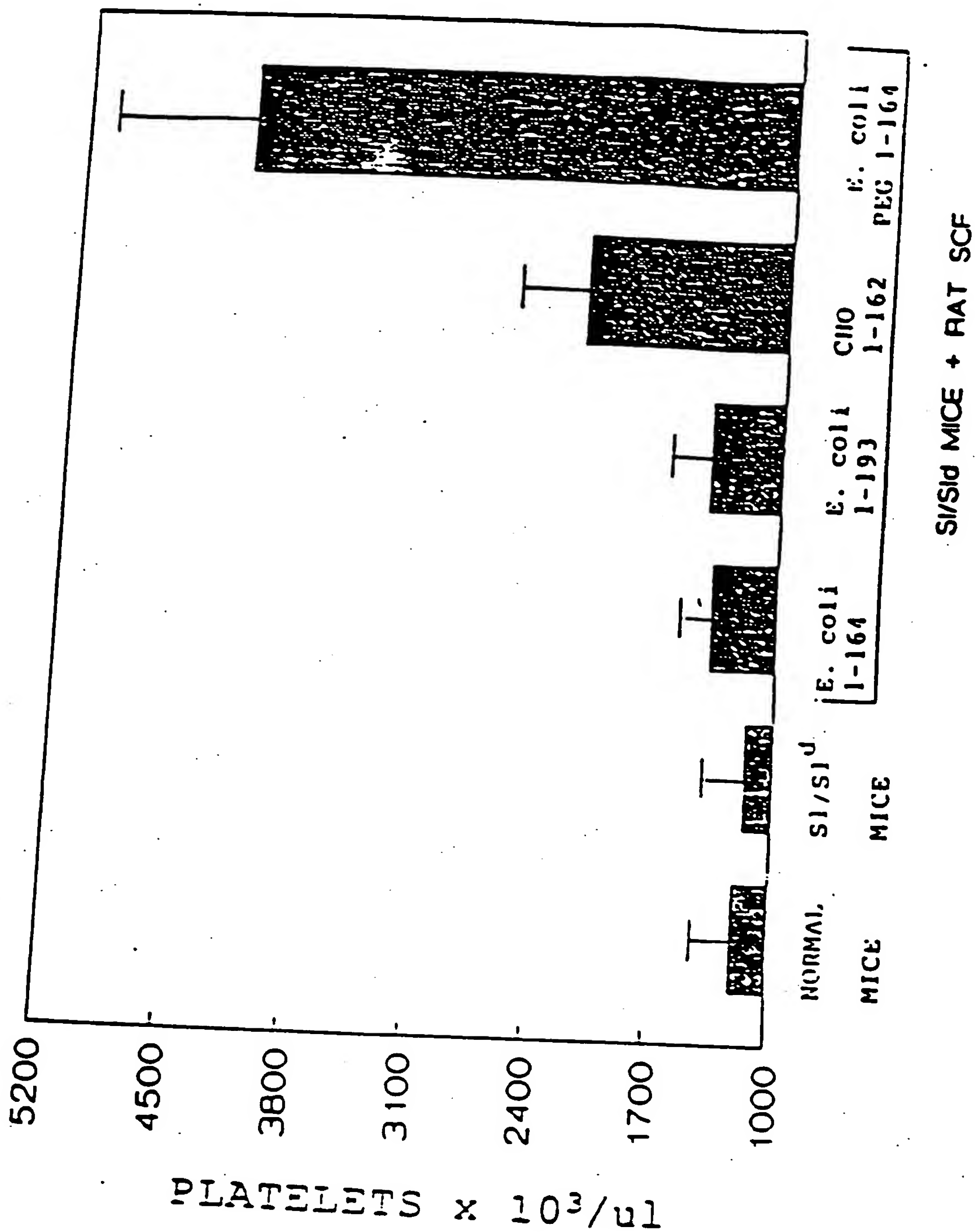

5200
4500
3800
3100
2400
1700
1000
PLATELETS x 10³/ul
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 27

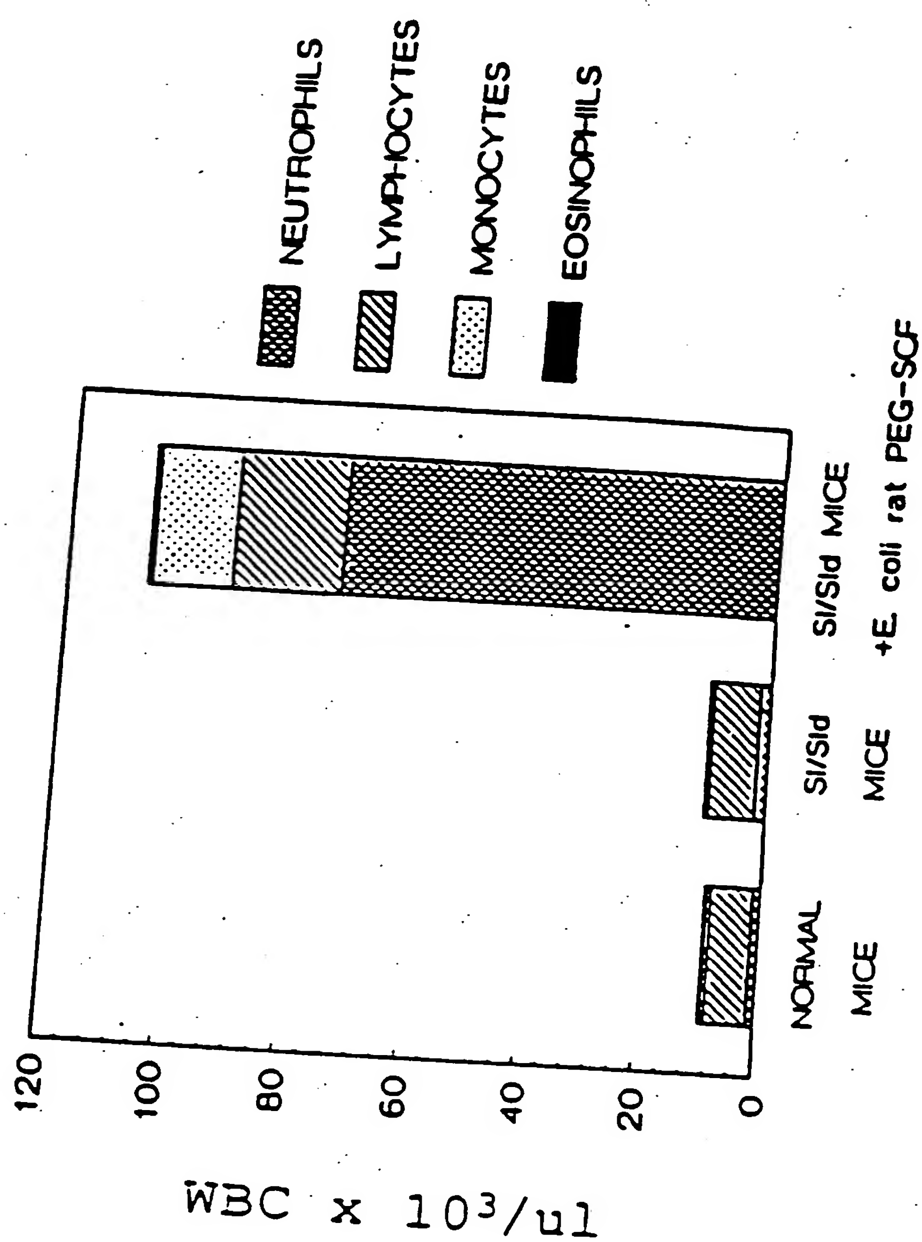

NEUTROPHILS
LYMPHOCYTES
MONOCYTES
EOSINOPHILS
120
100
80
60
40
20
0
WBC x 10³/ul
NORMAL MICE
Sl/Sld MICE
Sl/Sld MICE +E. coli rat PEG-SCF

FIG. 28

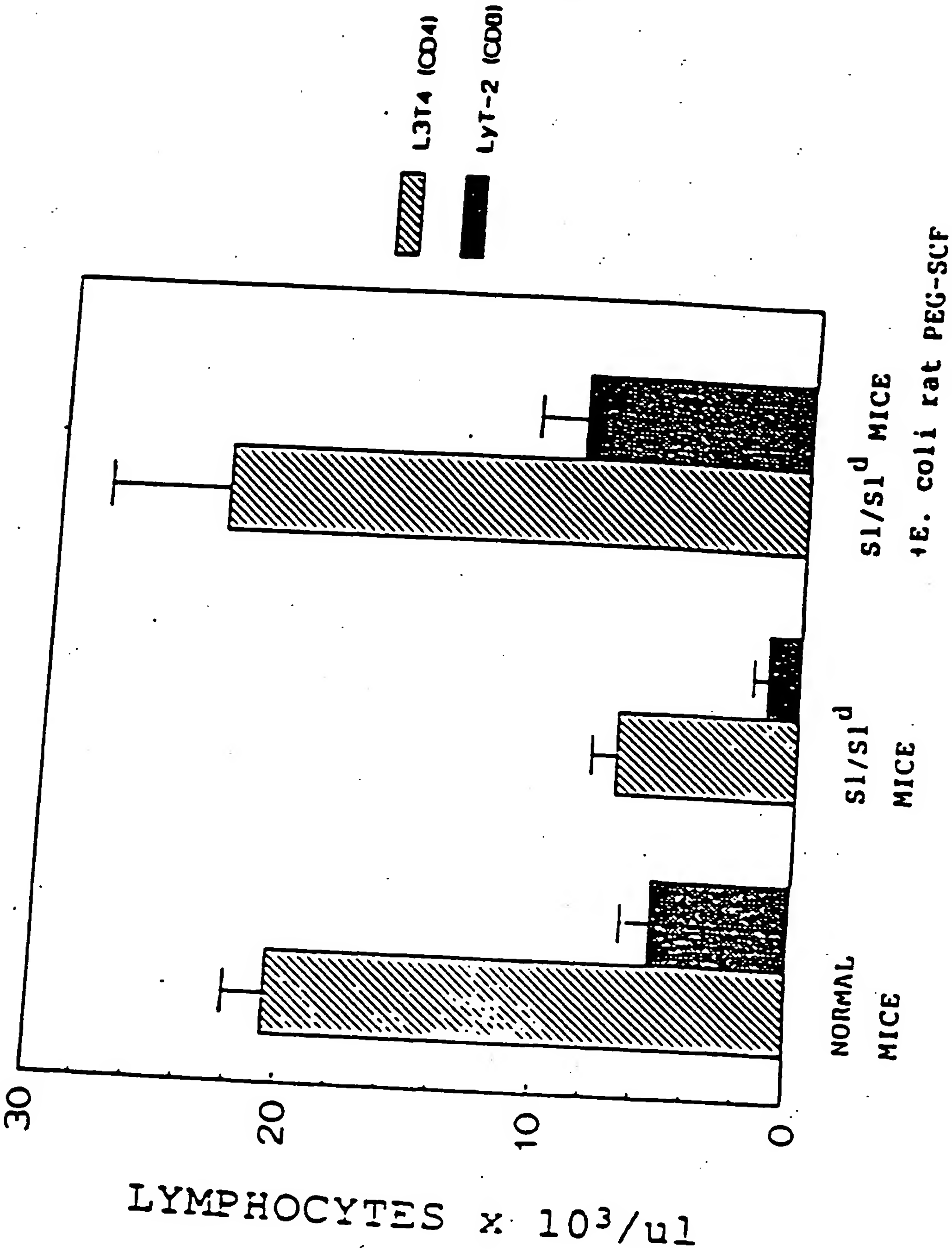

L3T4 (CD4)
LyT-2 (CD8)
30
20
10
0
LYMPHOCYTES x 10³/ul
NORMAL MICE
Sl/Sl^d MICE
Sl/Sl^d MICE +E. coli rat PEG-SCF

FIG. 29A

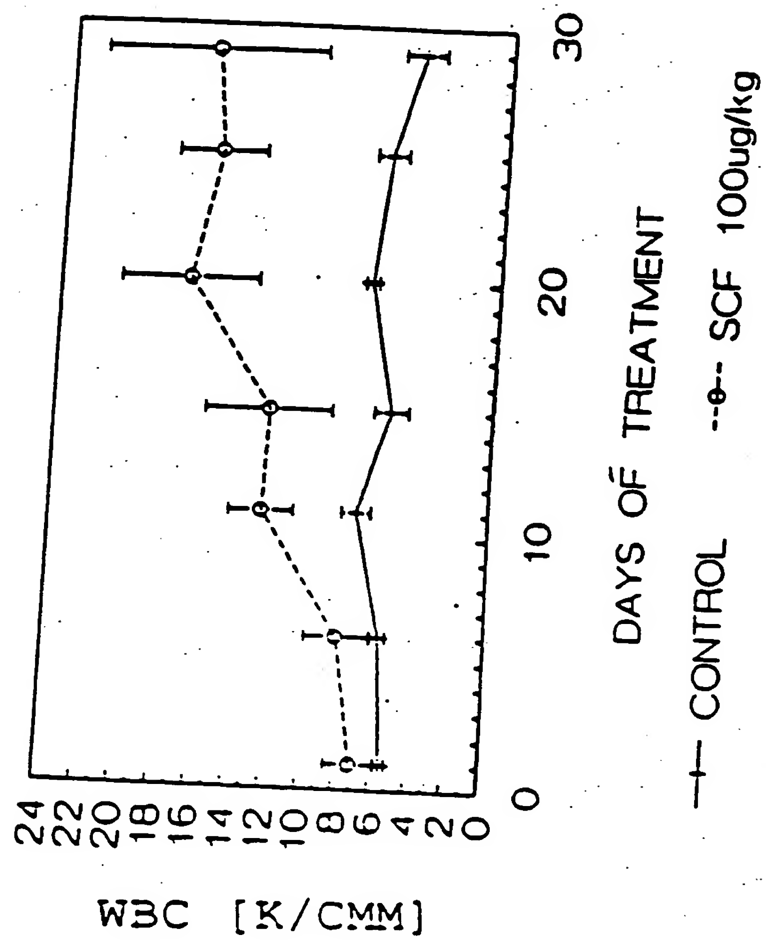

WBC [K/CMM]
24
22
20
18
16
14
12
10
8
6
4
2
0
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.29B

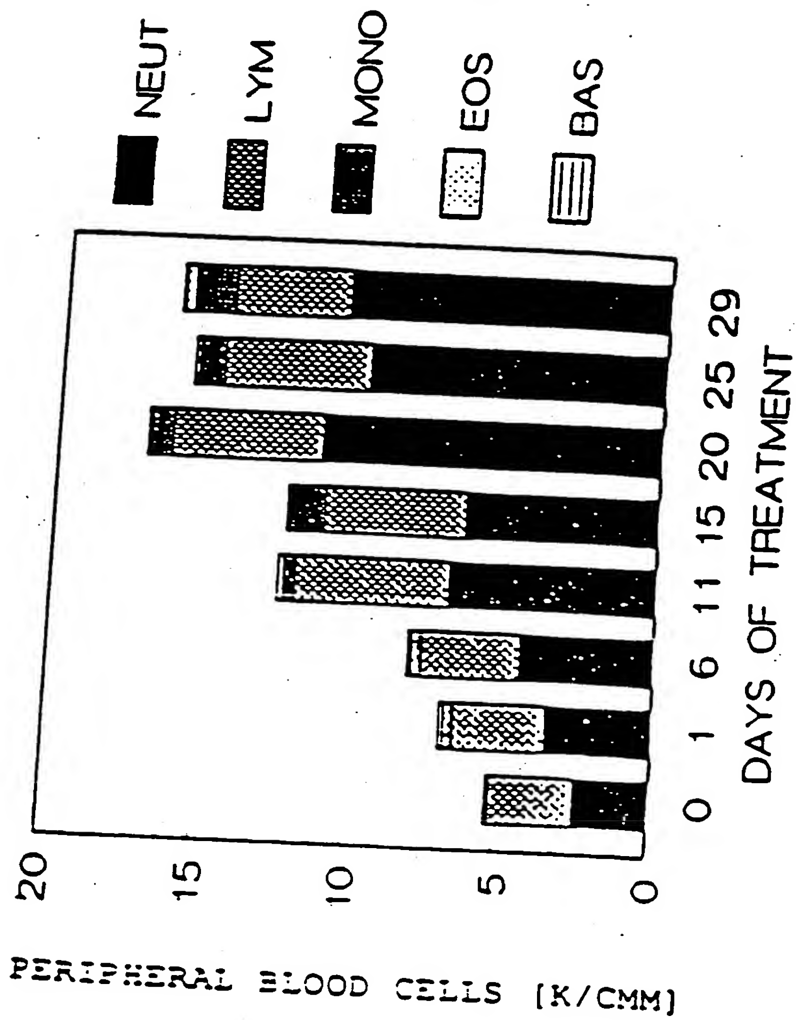

NEUT
LYM
MONO
EOS
BAS
0 1 6 11 15 20 25 29
DAYS OF TREATMENT
20
15
10
5
0
PERIPHERAL BLOOD CELLS [K/CMM]

FIG.30A

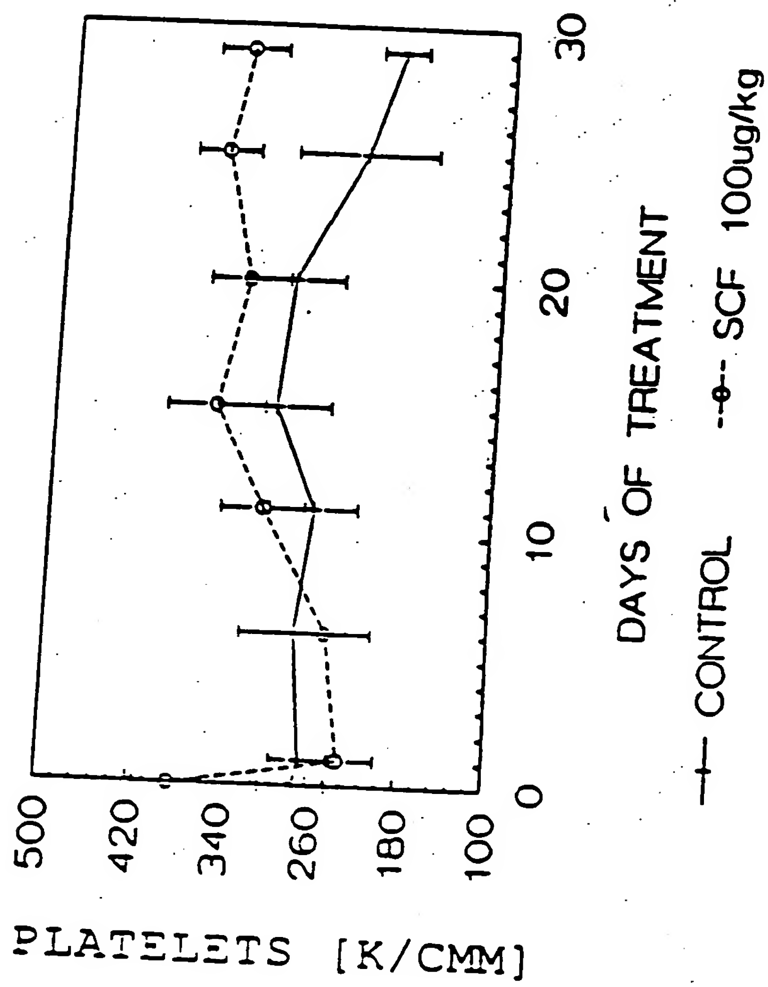
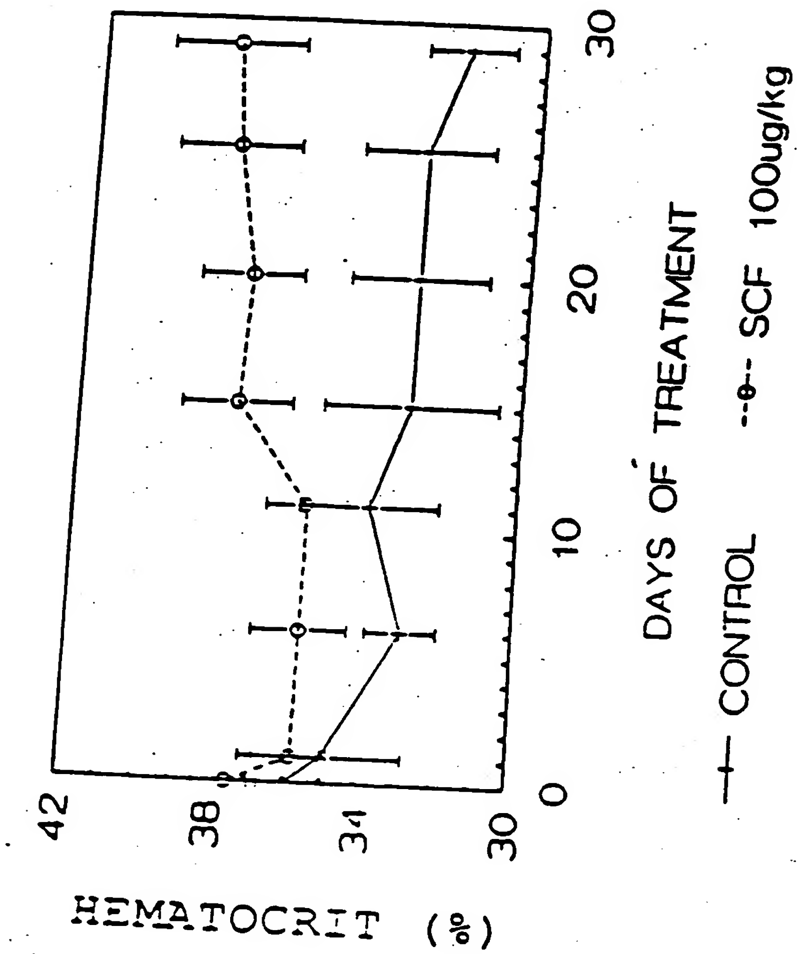

500
420
340
260
180
100
PLATELETS [K/CMM]
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.30B


HEMATOCRIT (%)
42
38
34
30
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

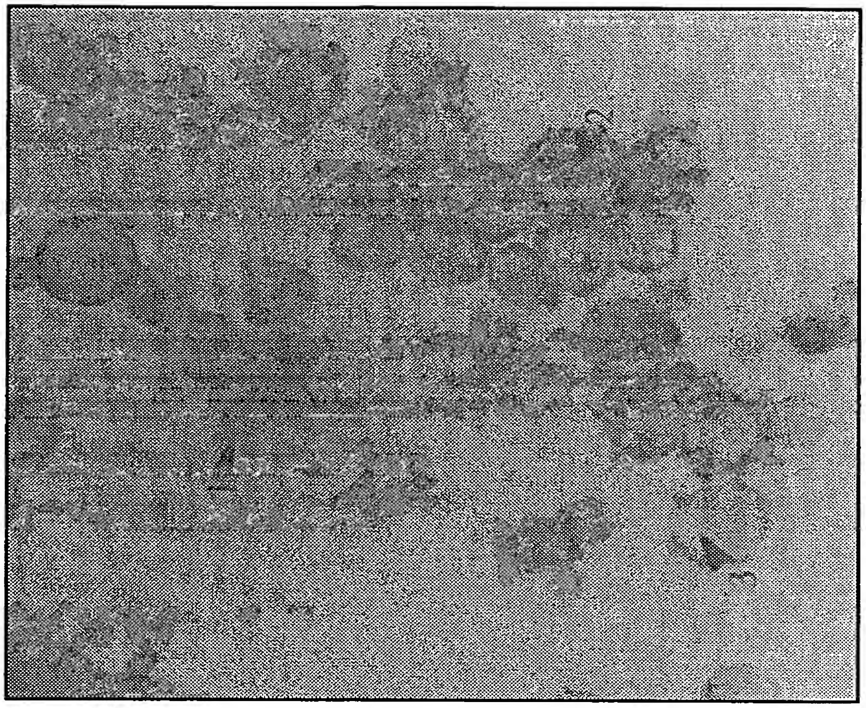


FIG. 31B

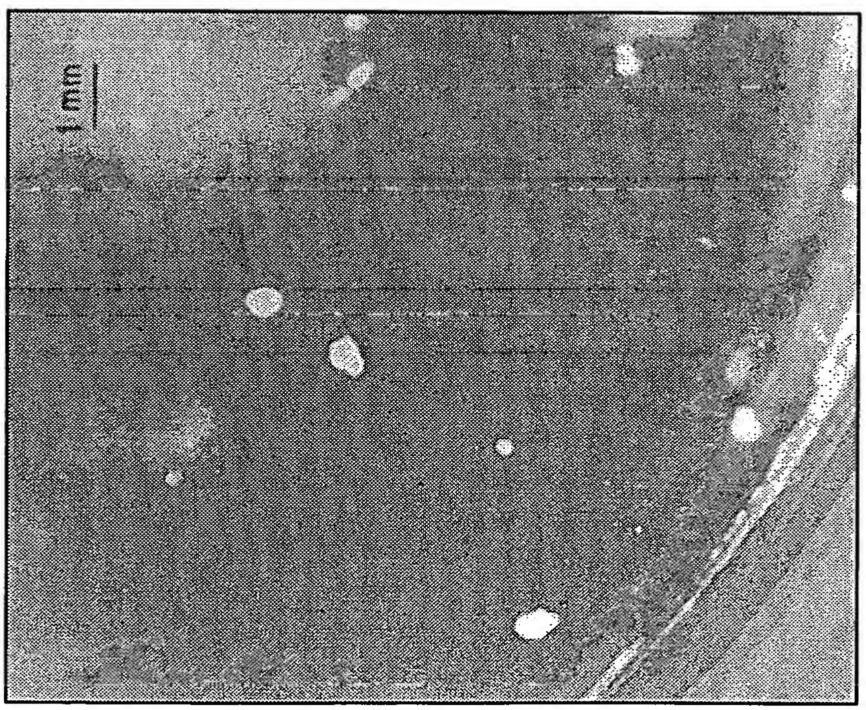


FIG. 31A

FIG. 31C

SCF4 SMP4

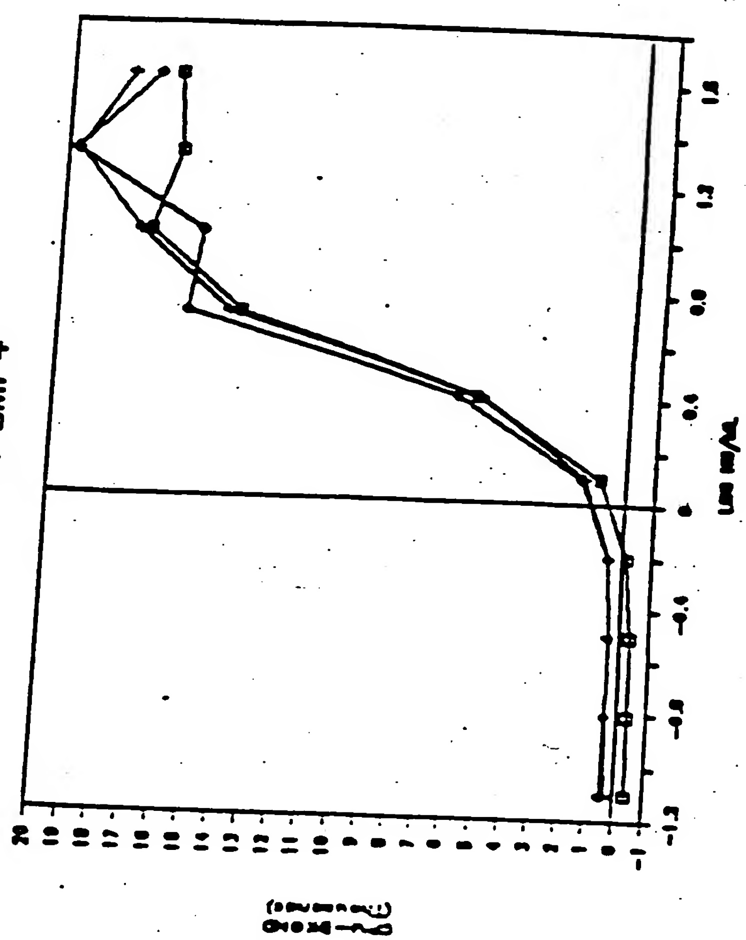


FIG. 32A

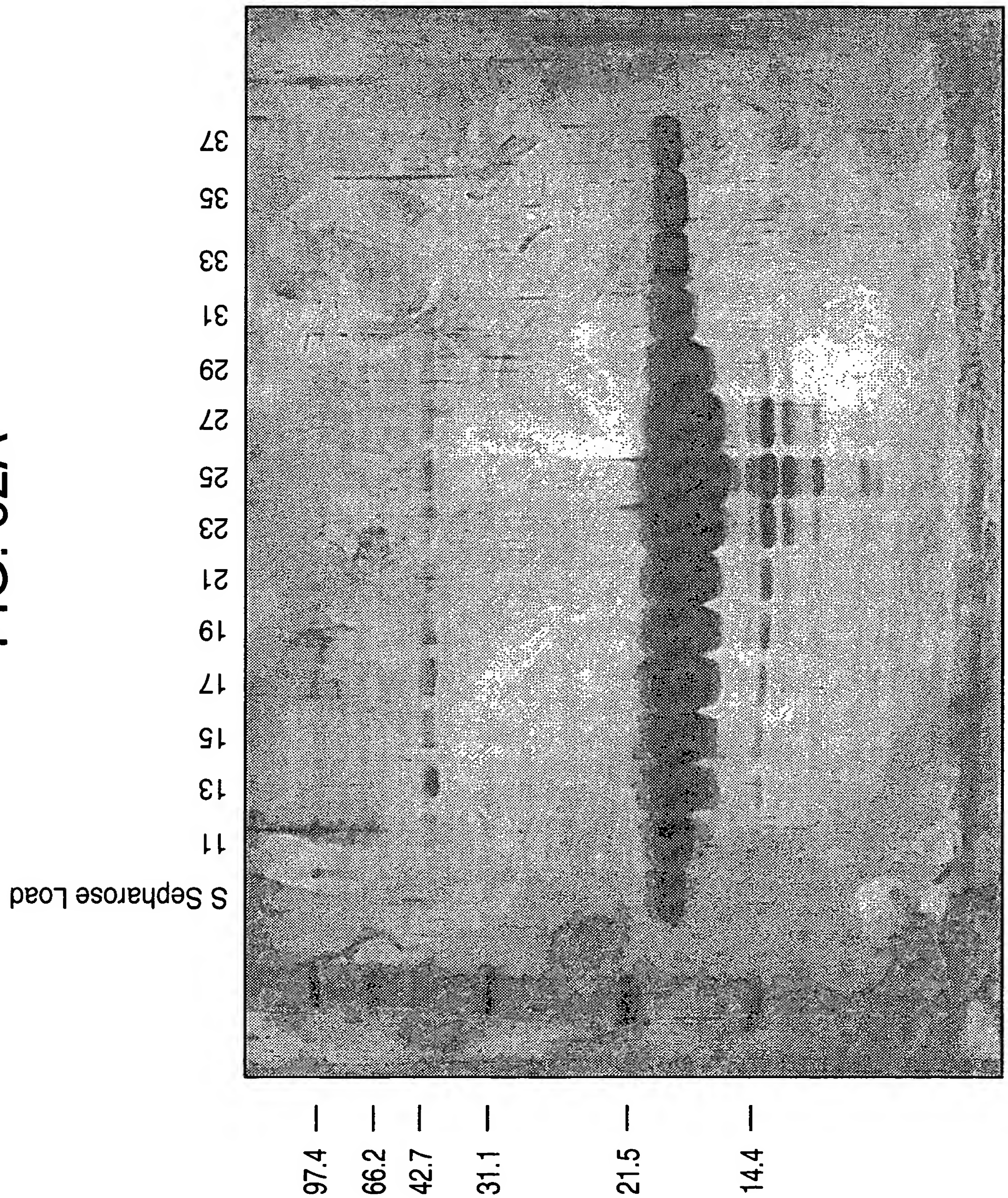

S Sepharose Load
11
13
15
17
19
21
23
25
27
29
31
33
35
37
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 32B

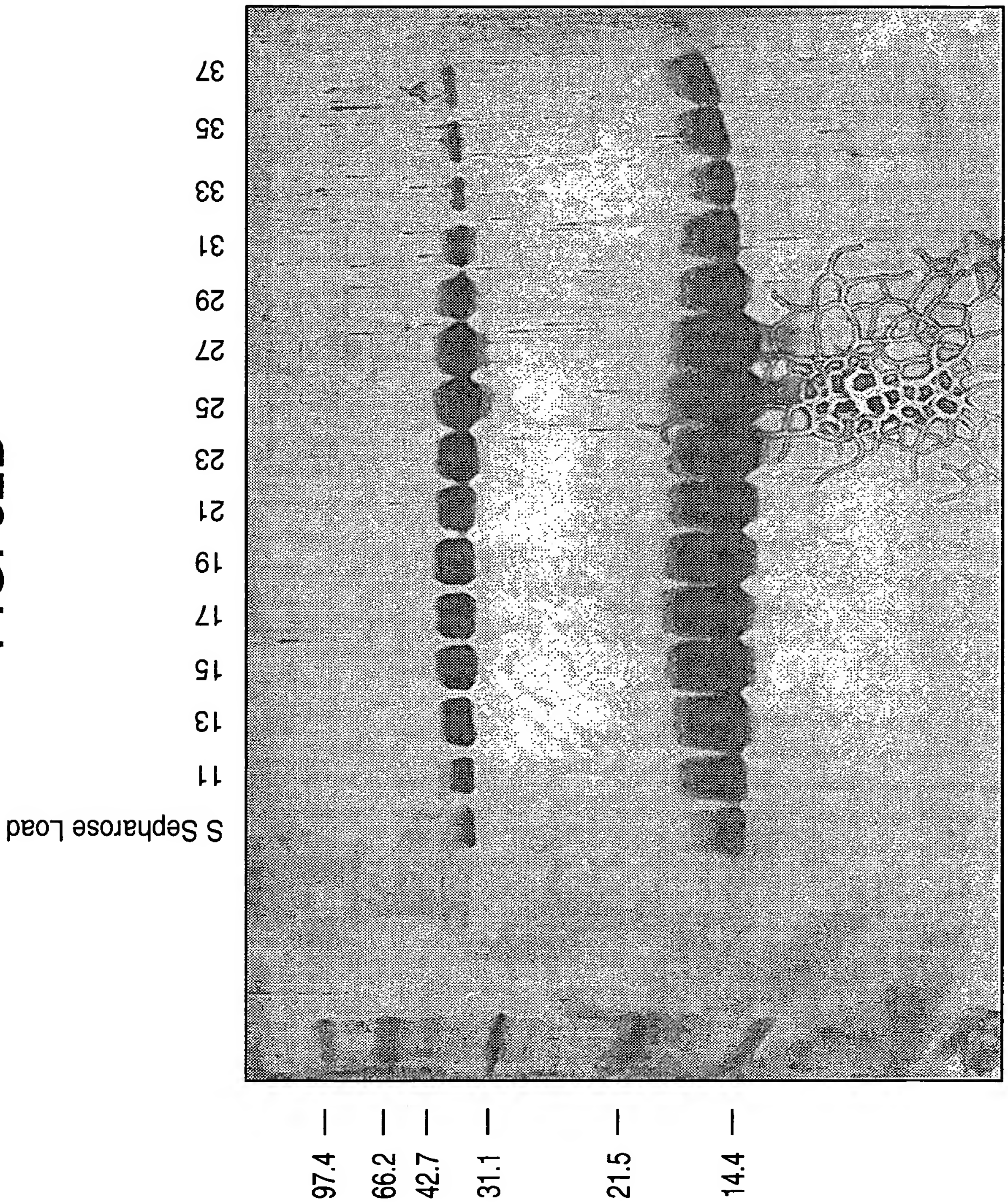

S Sepharose Load
11
13
15
17
19
21
23
25
27
29
31
33
35
37
97.4
66.2
42.7
31.1
21.5
14.4

FIG.33

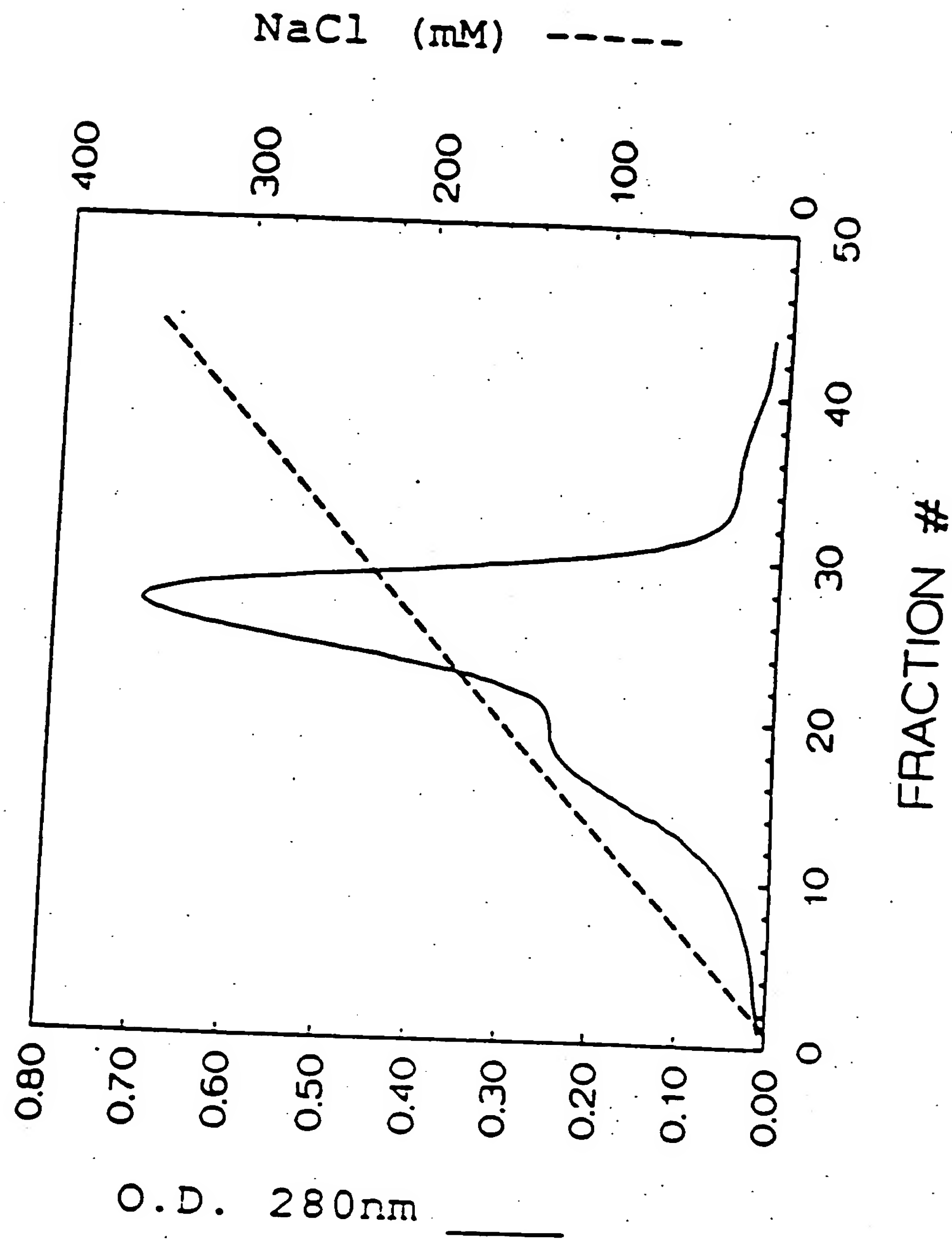

NaCl (mM)
400
300
200
100
0
50
40
30
20
10
0
FRACTION #
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
O.D. 280nm

FIG. 34A

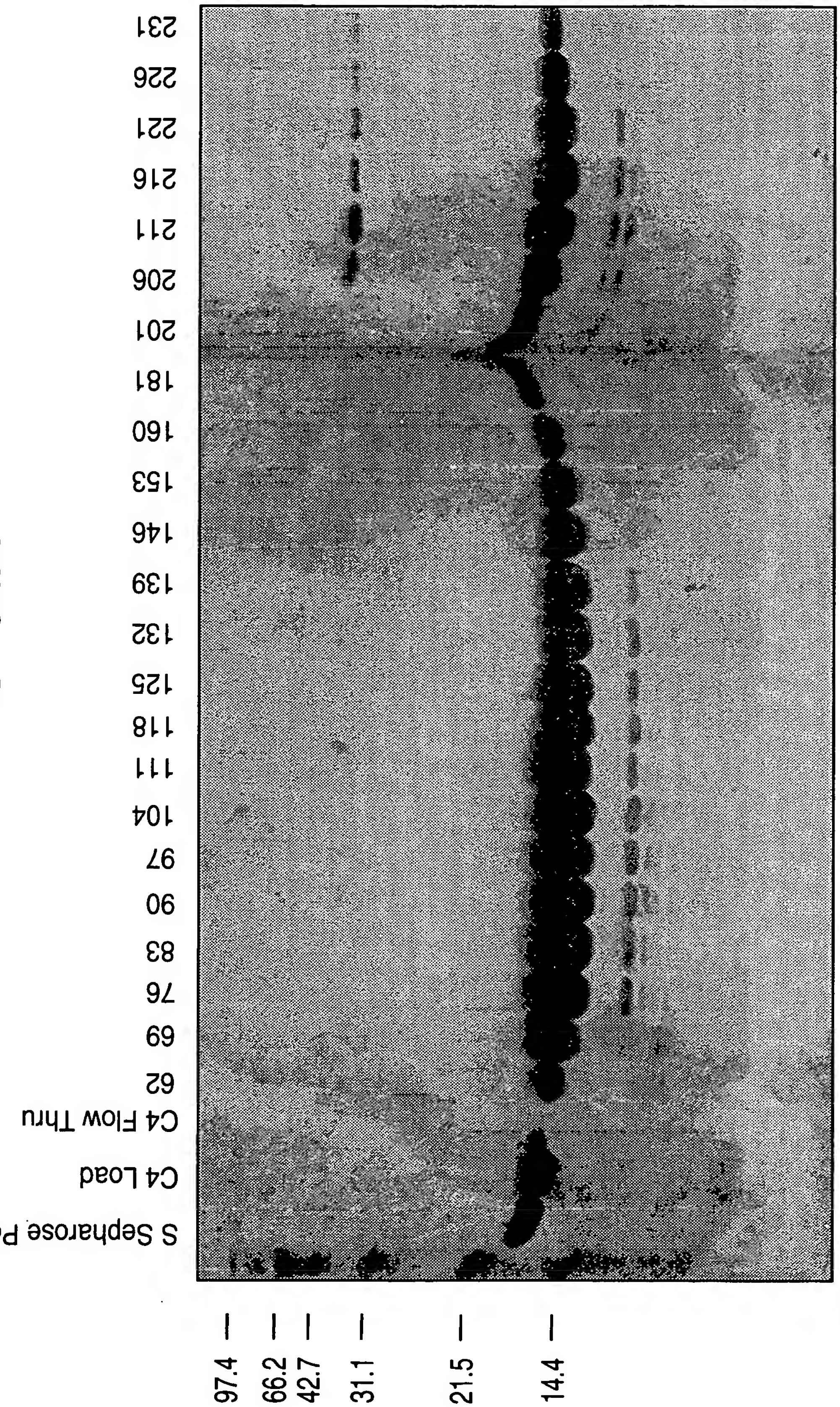

S Sepharose Pool
C4 Load
C4 Flow Thru
62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 34B

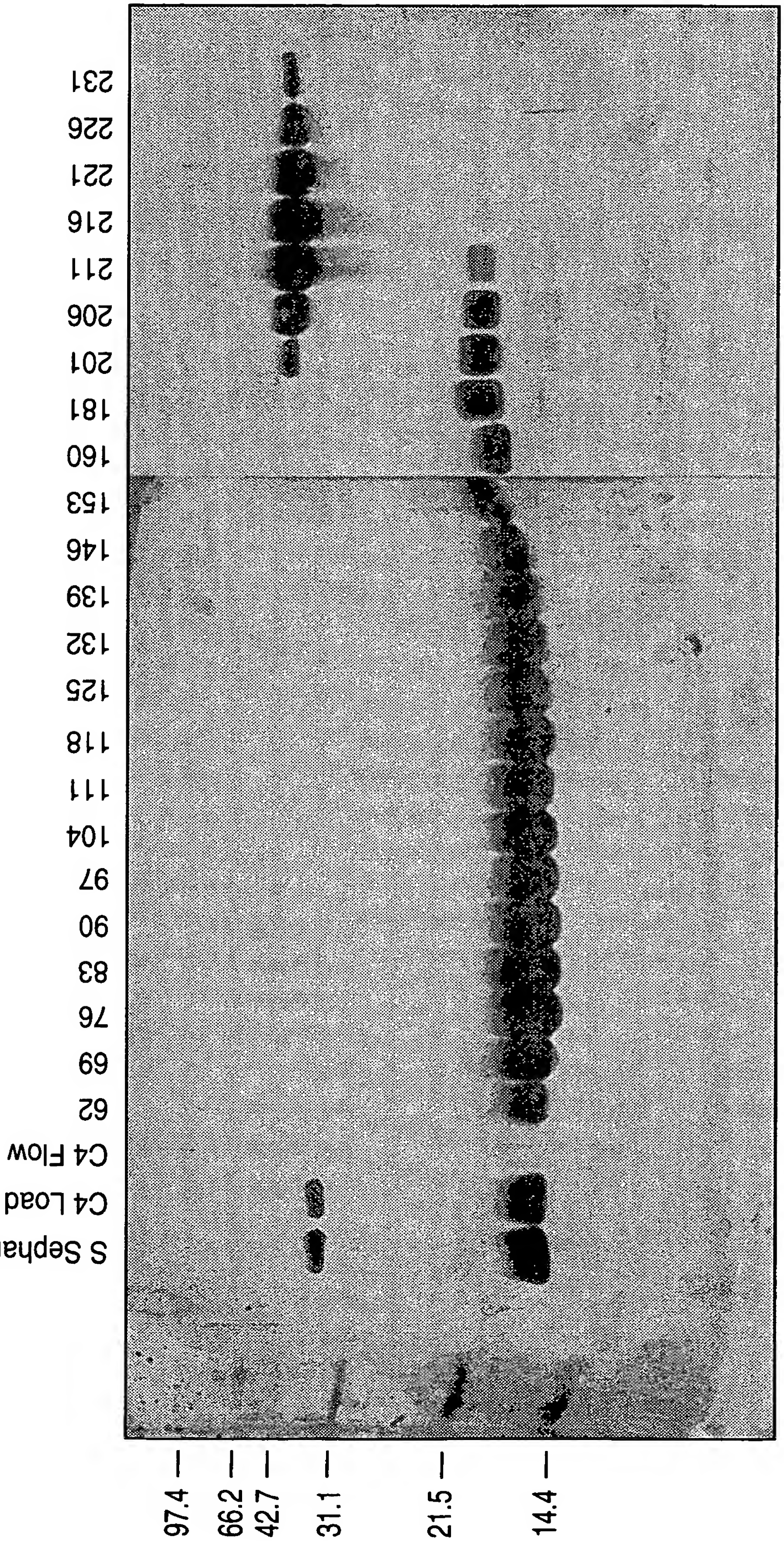

231
226
221
216
211
206
201
181
160
153
146
139
132
125
118
111
104
97
90
83
76
69
62
C4 Flow Thru
C4 Load
S Sepharose Pool
97.4
66.2
42.7
31.1
21.5
14.4

FIG.35

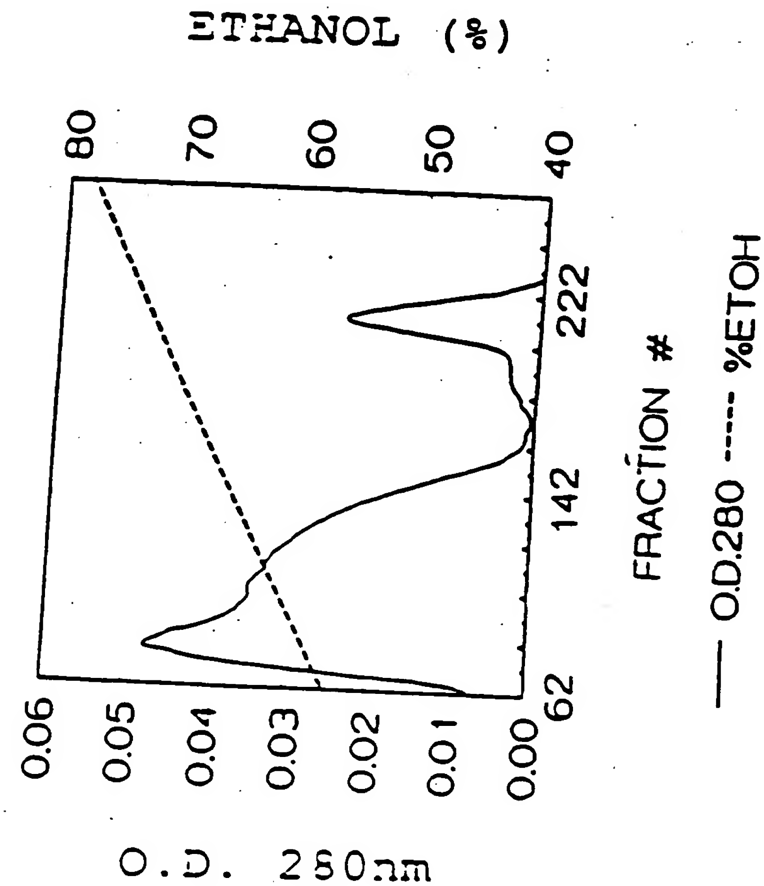

ETHANOL (%)
80
70
60
50
40
222
142
62
FRACTION #
— O.D.280 ----- %ETOH
0.06
0.05
0.04
0.03
0.02
0.01
0.00
O.D. 280nm

FIG. 36

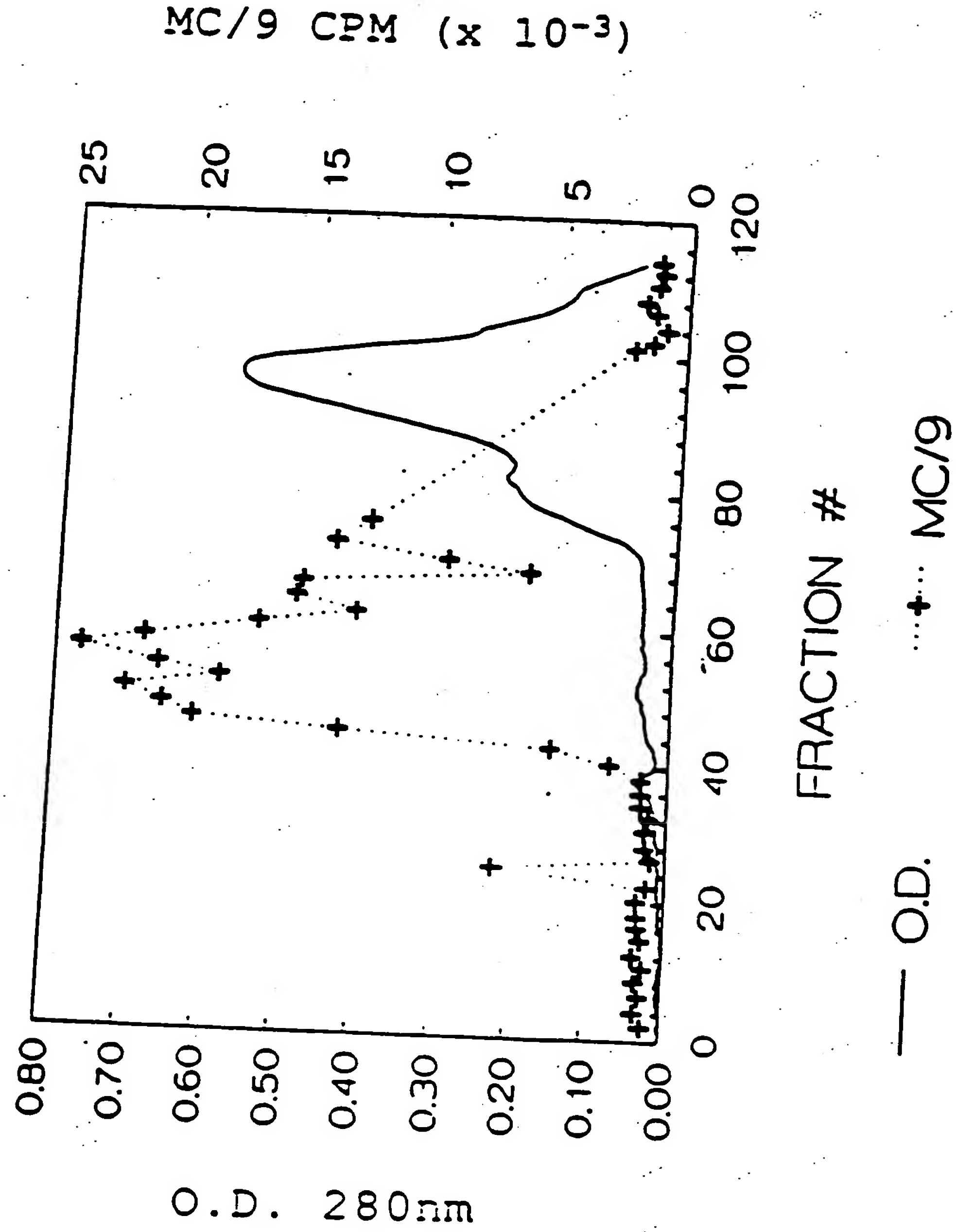
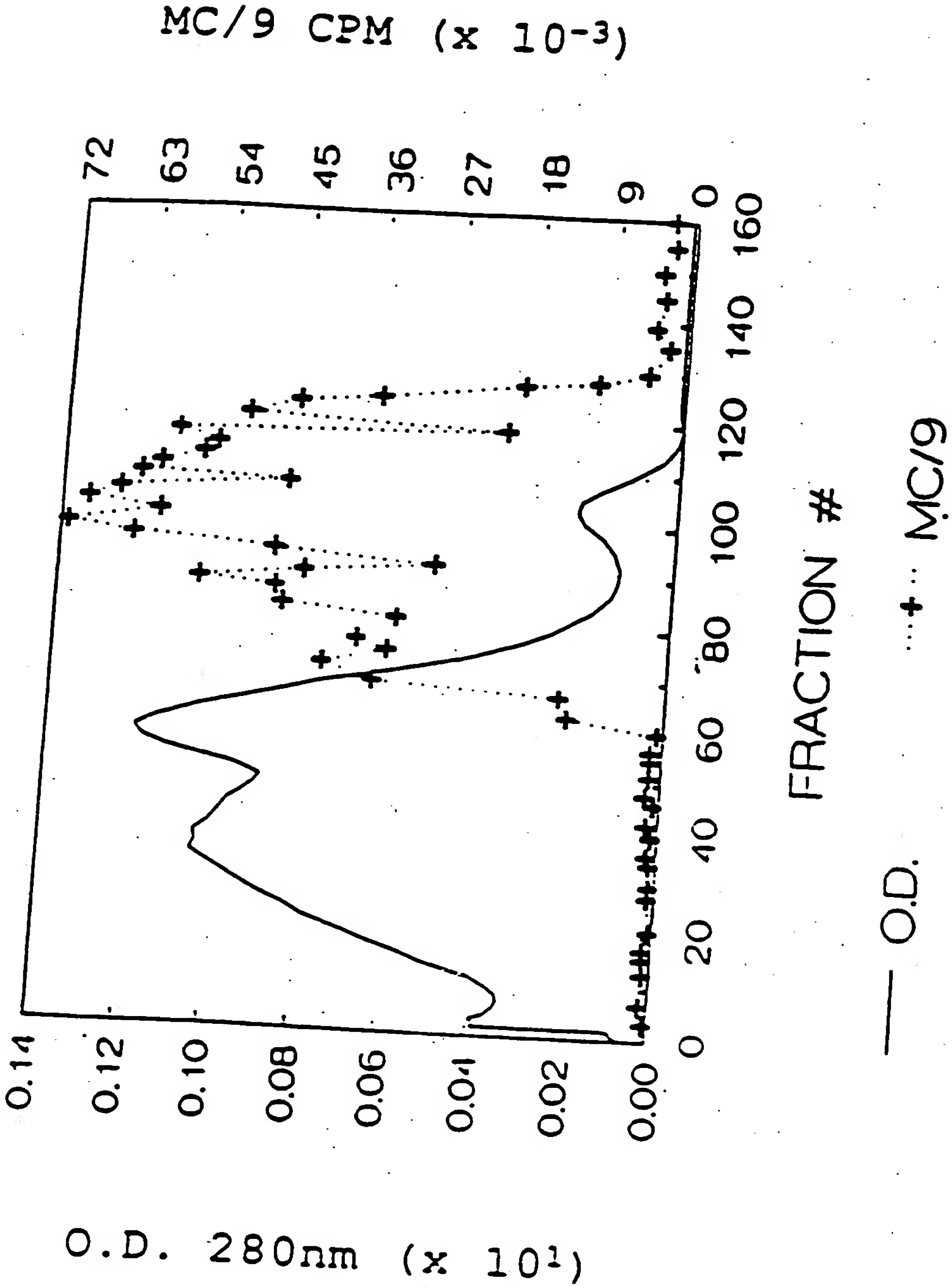

MC/9 CPM (x 10^{-3})
25
20
15
10
5
0
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0
20
40
60
80
100
120
FRACTION #
— O.D.
··+·· MC/9
O.D. 280nm

FIG. 37


MC/9 CPM (x 10^{-3})
72
63
54
45
36
27
18
9
0
160
140
120
100
80
60
40
20
0
FRACTION #
— O.D.
···+··· MC/9
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
O.D. 280nm (x 10^{1})

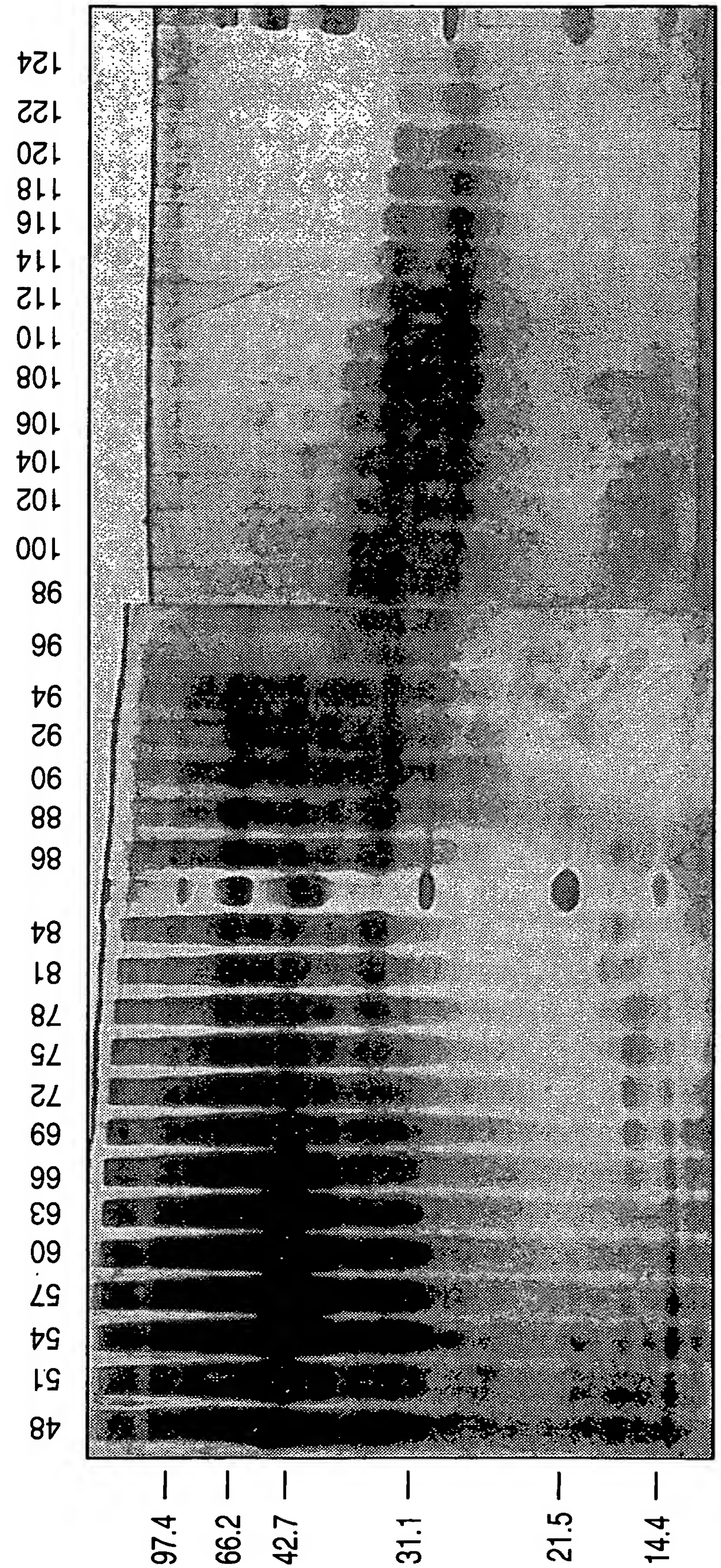

48
51
54
57
60
63
66
69
72
75
78
81
84
86
88
90
92
94
96
98
100
102
104
106
108
110
112
114
116
118
120
122
124
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 38

FIG. 39

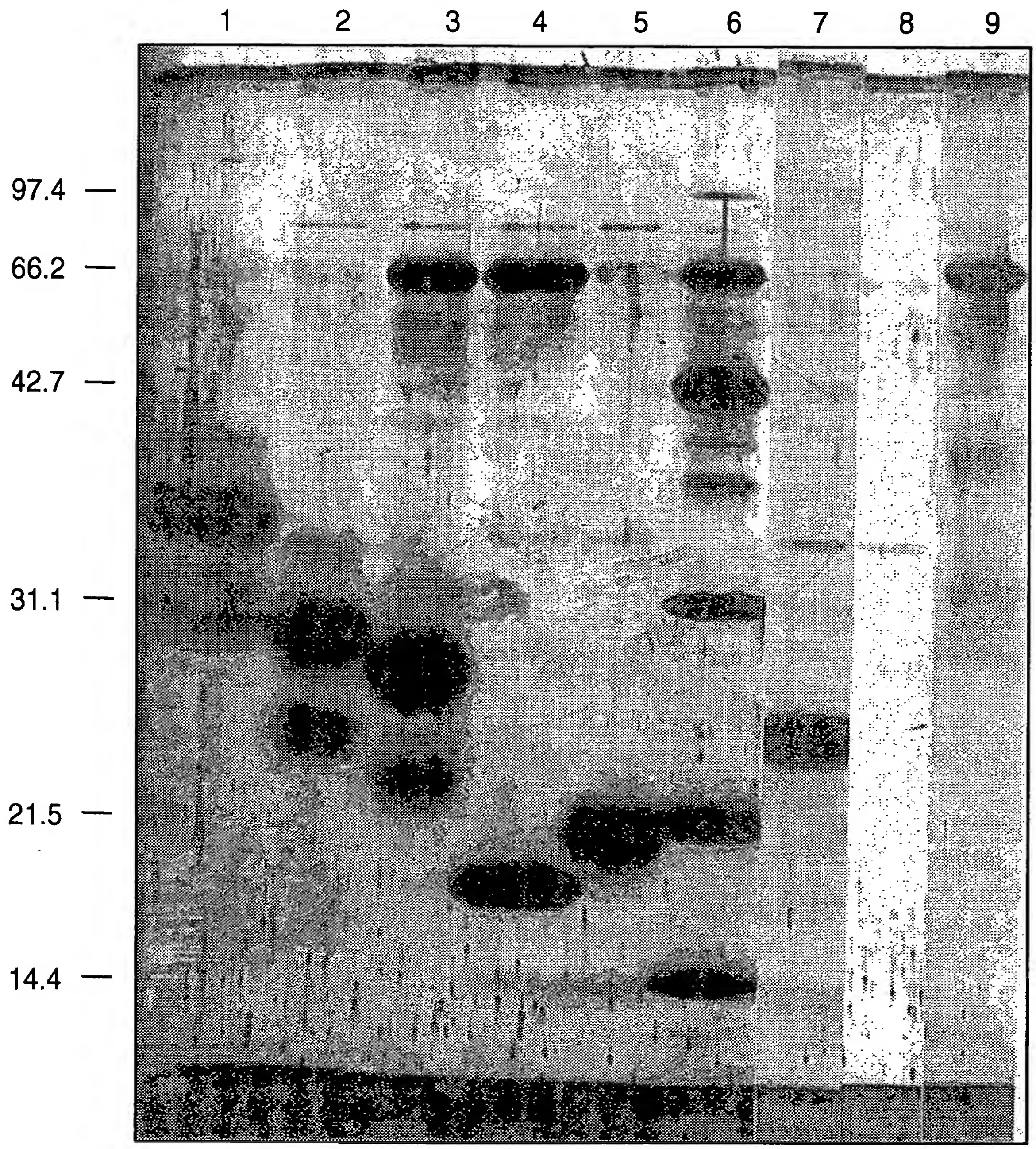


FIG. 40A

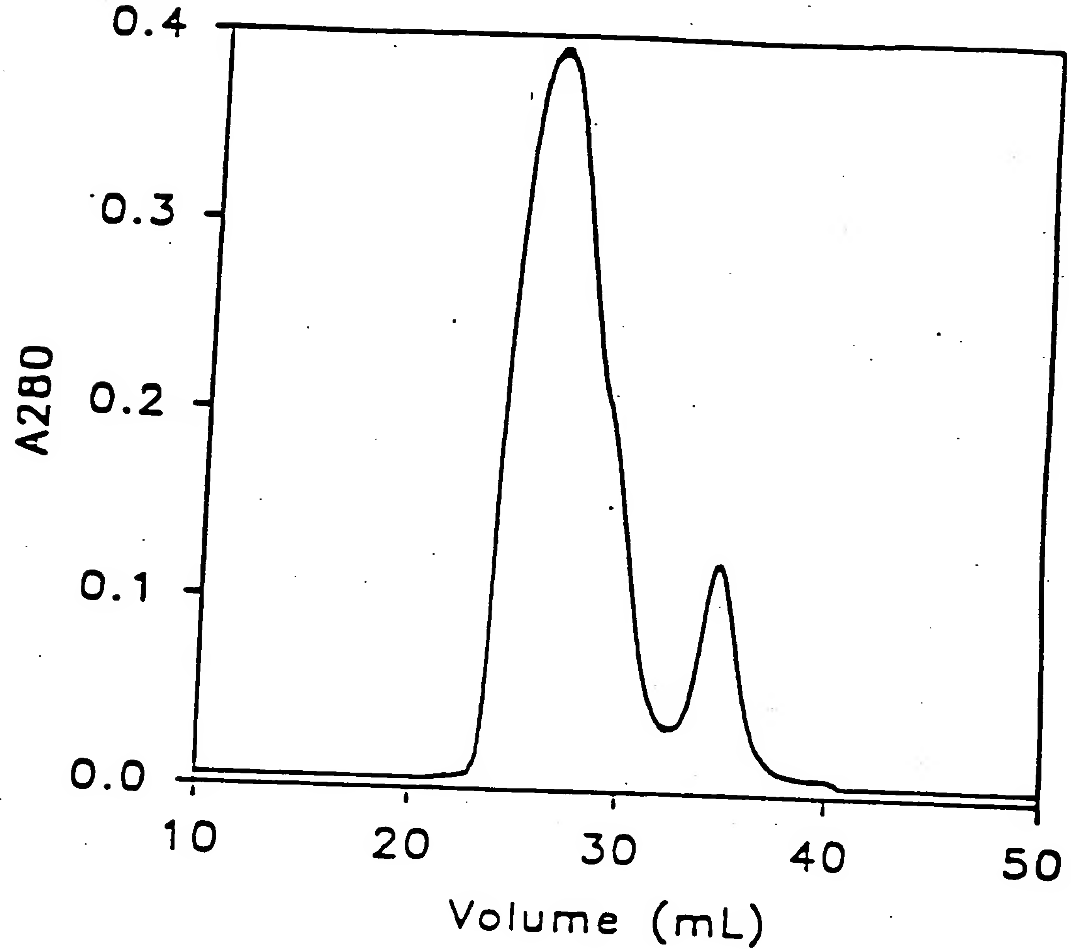


FIG. 40B

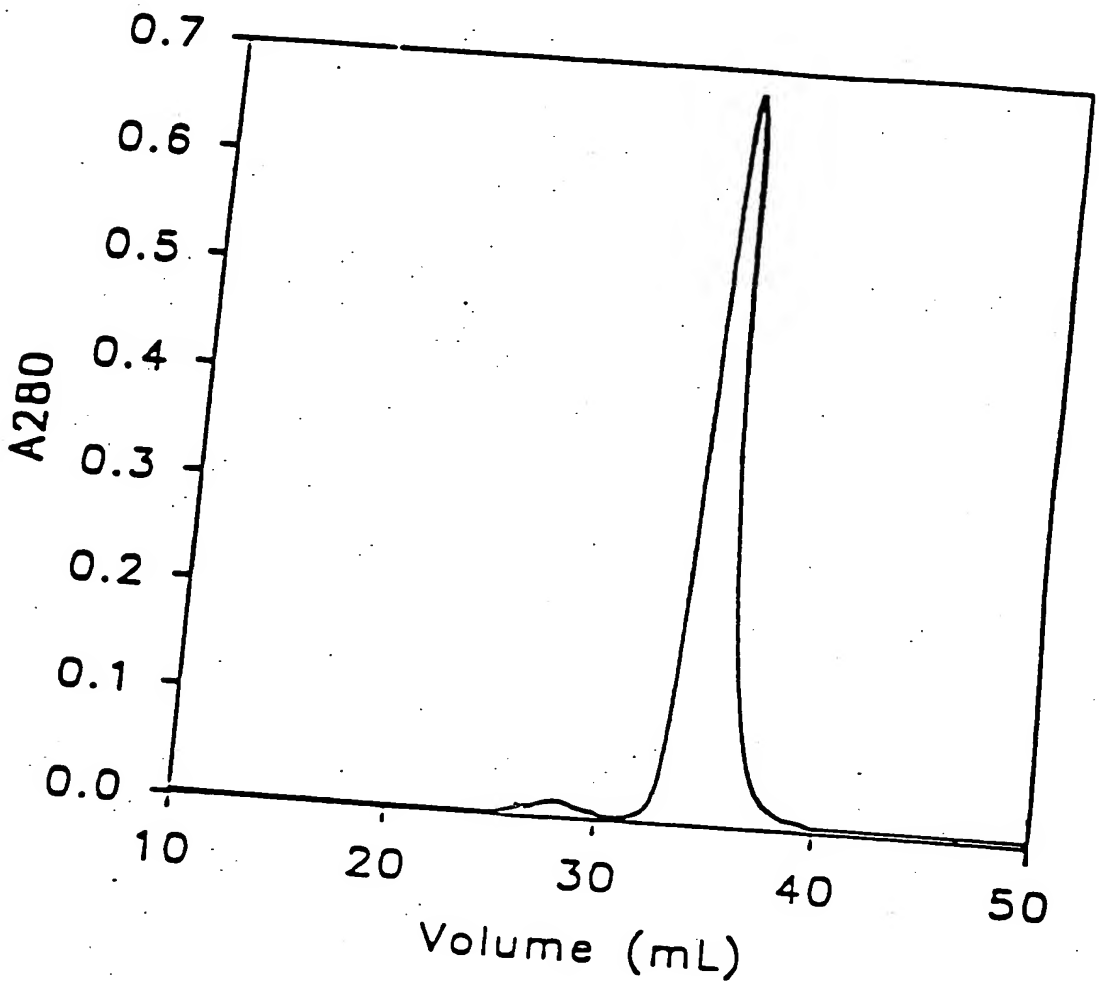


FIG. 41

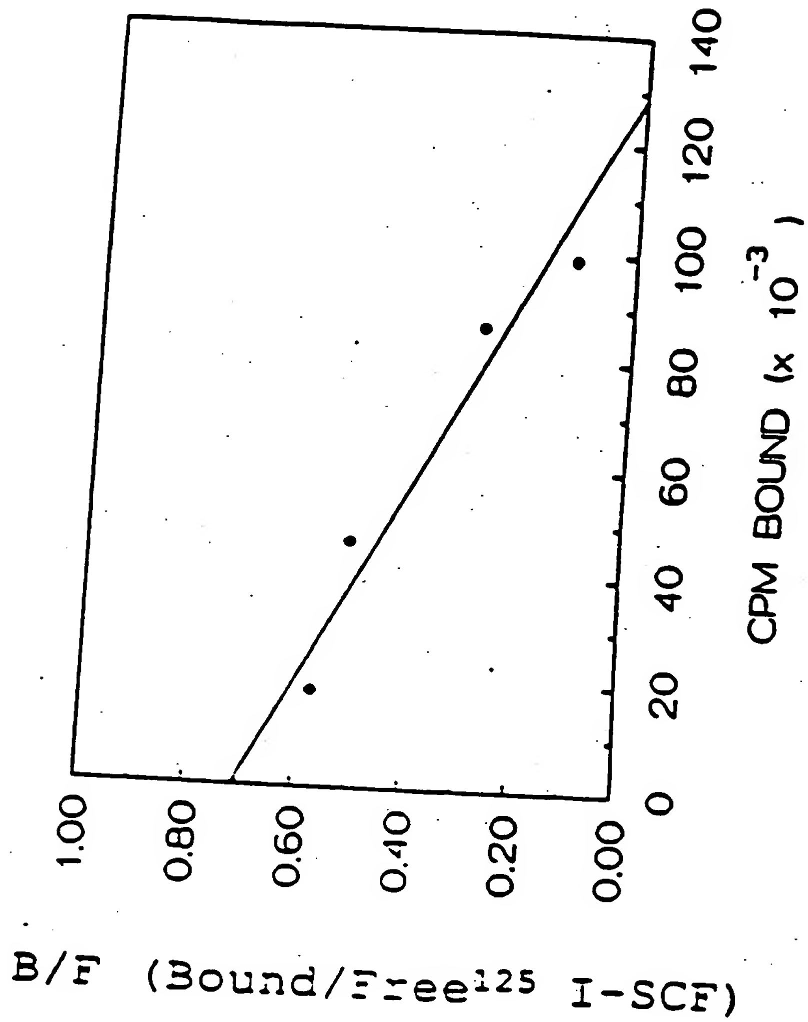

1.00
0.80
0.60
0.40
0.20
0.00
0
20
40
60
80
100
120
140
CPM BOUND (x 10^{-3})
B/F (Bound/Free^{125} I-SCF)

FIG. 42A

```
CCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGC   61

TCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA  122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  183

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG      228

-10                                     1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG      273

                10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA      318

                                    30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG      363

                40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA      408

                                    60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT      453
```

FIG. 42B

```
                    70                                              80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    498

                                     90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    543

                100                                        110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    588

                                     120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    633

                130                                        140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    678

                                     150
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA    723
```

FIG.42C

```
                    160                                                   170
Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT    768

                                        180
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC    813

                190                                                   200
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT    858

                                        210
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA    903

                220                                                   230
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA    948

                                    240
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT    993

        248
Gln Glu Val End
CAA GAA GTG TAA      TTGTGGCTTGTATCAACACTGTTACTTTCGTACATTGGC 1044
```

FIG. 42D

```
TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104
TGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164
AGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224
GAACTTGCATGGAGCAGGACTCTATTTTAAGGACTGCGGGACTTGGGTCTCATTTAGAAC 1284
TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344
TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404
```

FIG. 43

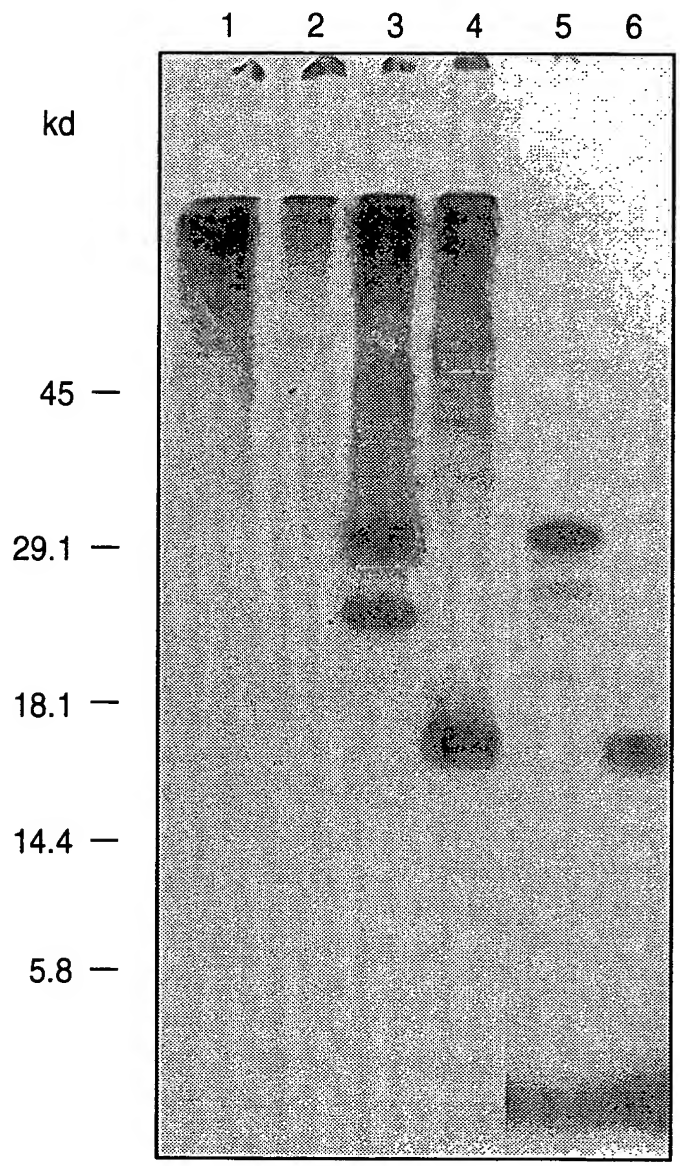


FIG. 44A

```
                                AGCAGGGACAGTGGAGAGGGCGCTGCGCTC   30
GGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCAG   90
AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  150

-25            -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG  195

-10                                      1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG  240

                10                                       20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA  285

                                     30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG  330

                40                                       50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA  375
```

FIG. 44B

```
                                           60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    420

                 70                                     80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    465

                                       90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    510

                100                                     110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    555

                                    120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    600

                130                                     140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    645

                                    150
Ser Ser Thr Leu Ser Pro Glu Lys|Gly|Lys Ala Lys Asn Pro Pro
TCT TCA ACA TTA AGT CCT GAG AAA|GGG|AAG GCC AAA AAT CCC CCT    690
```

FIG. 44C

```
                    160                                                 170
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu
GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG     735

                                    180
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG     780

                    190                                         200
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT     825

                                    210
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA     870

                    220
Glu Phe Gln Glu Val End
GAG TTT CAA GAA GTG TAA     TTGTGGCTTGTATCAACACTGTTACTTTCGTA     920

CATTGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATA     980

TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG    1040

ATGATTCAGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGA                1088
```

FIG. 45

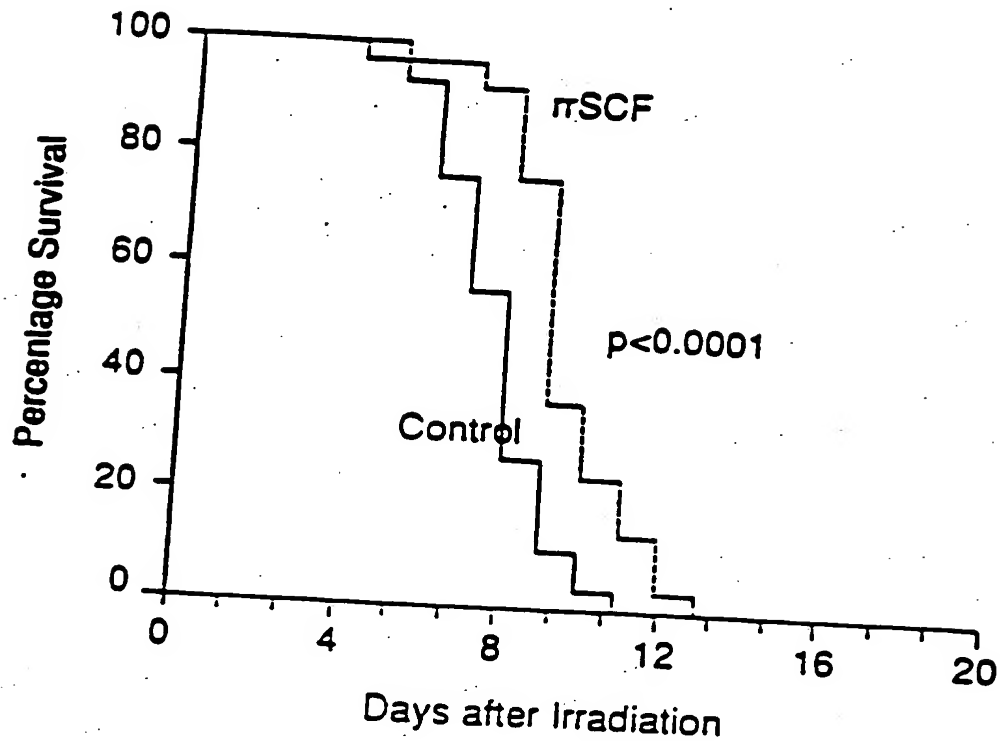
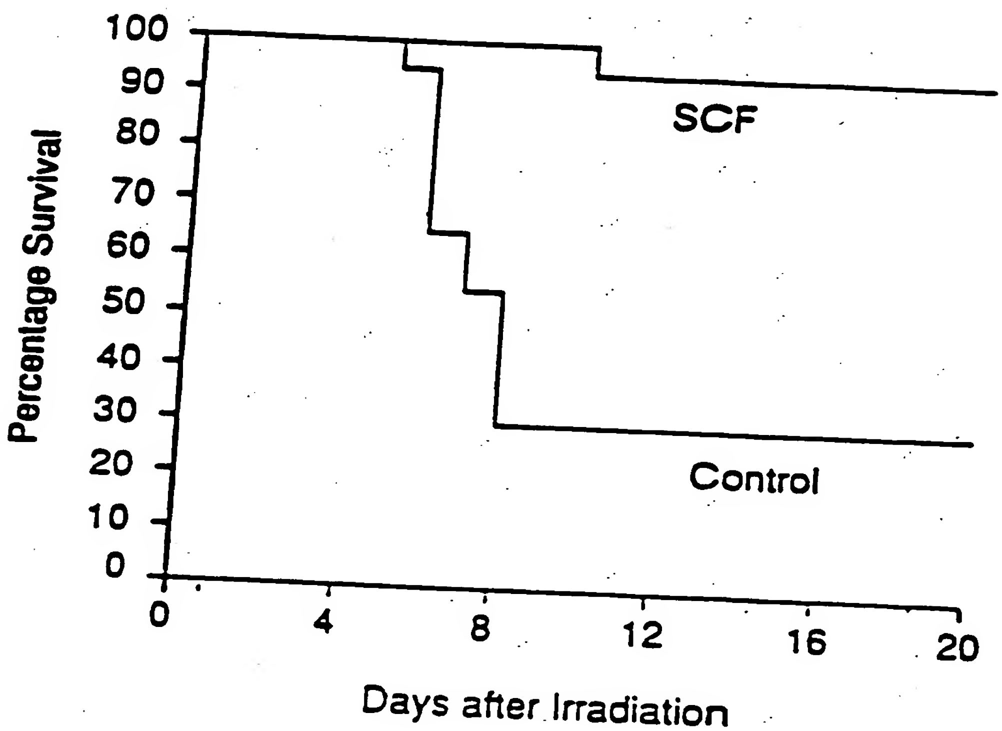

100
80
60
40
20
0
Percenlage Survival
rrSCF
p<0.0001
Control
0
4
8
12
16
20
Days after Irradiation

FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47

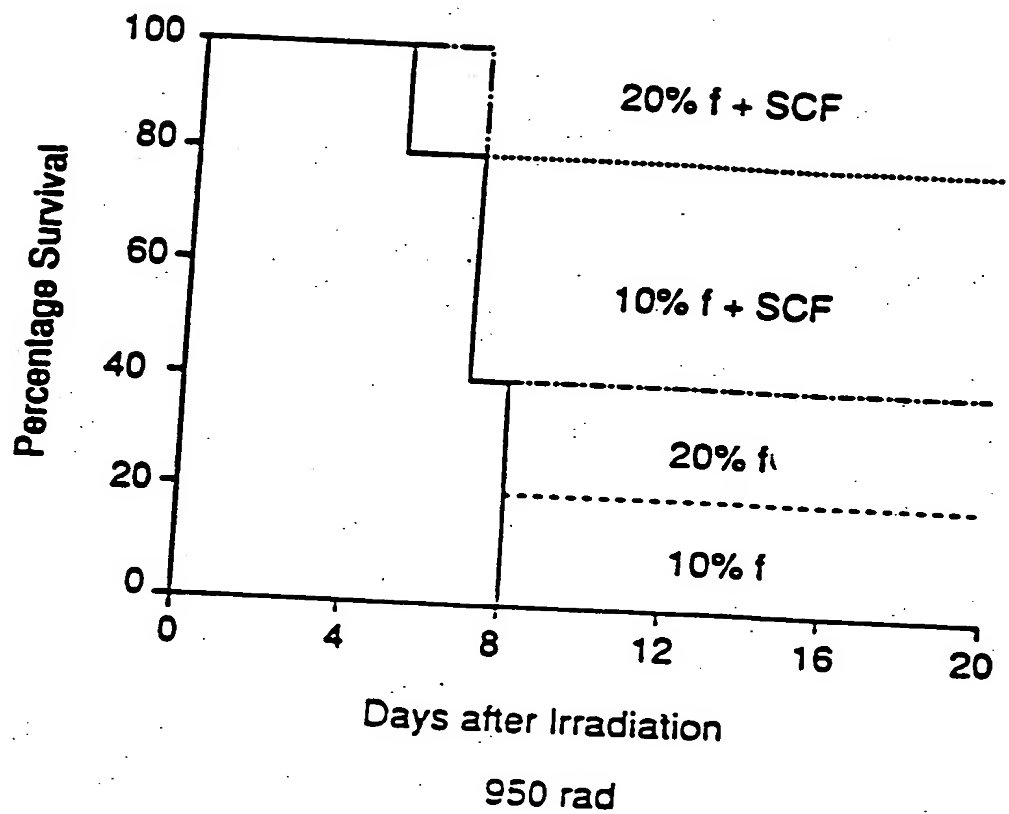

100
80
60
40
20
0
Percentage Survival
20% f + SCF
10% f + SCF
20% f
10% f
0
4
8
12
16
20
Days after Irradiation
950 rad

FIG. 48

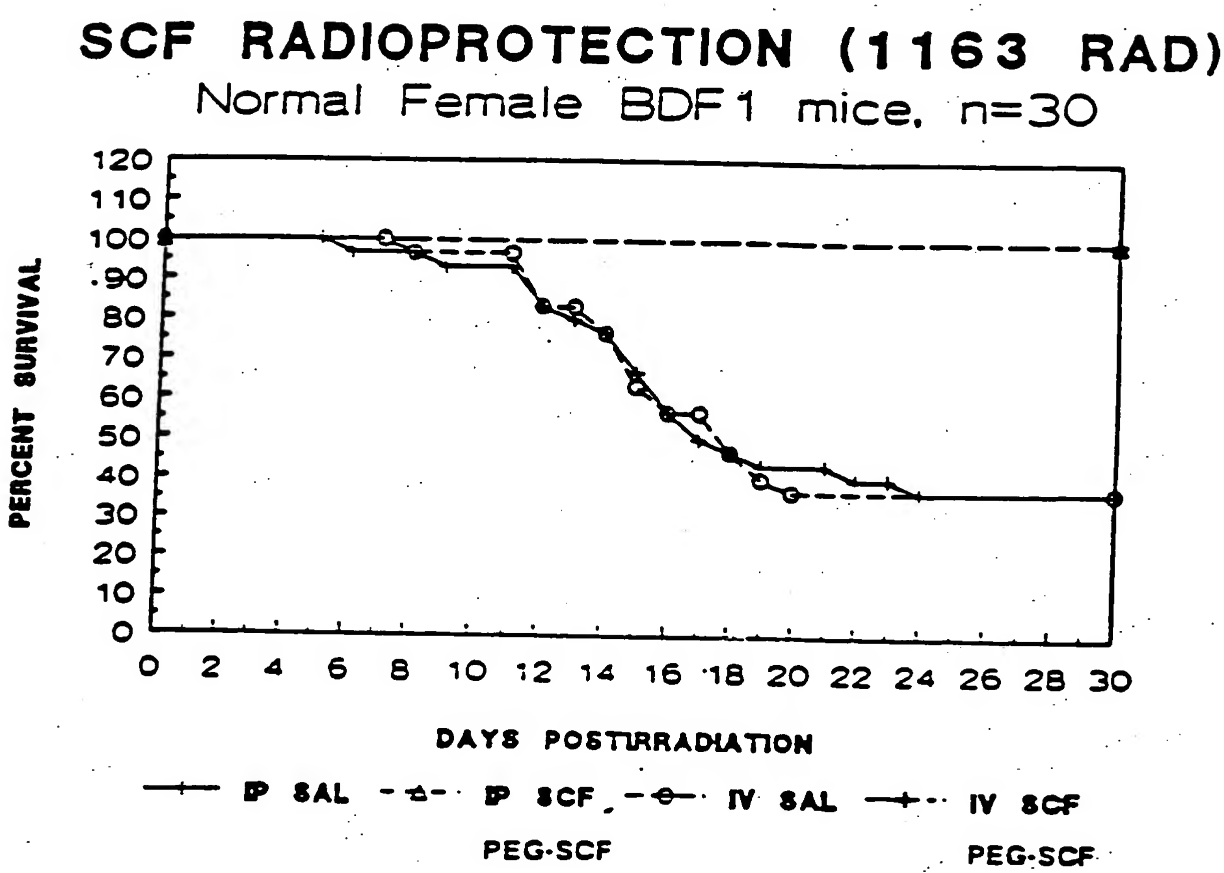

SCF RADIOPROTECTION (1163 RAD)
Normal Female BDF1 mice, n=30
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
DAYS POSTIRRADIATION
IP SAL
IP SCF
PEG-SCF
IV SAL
IV SCF
PEG-SCF

FIG. 49

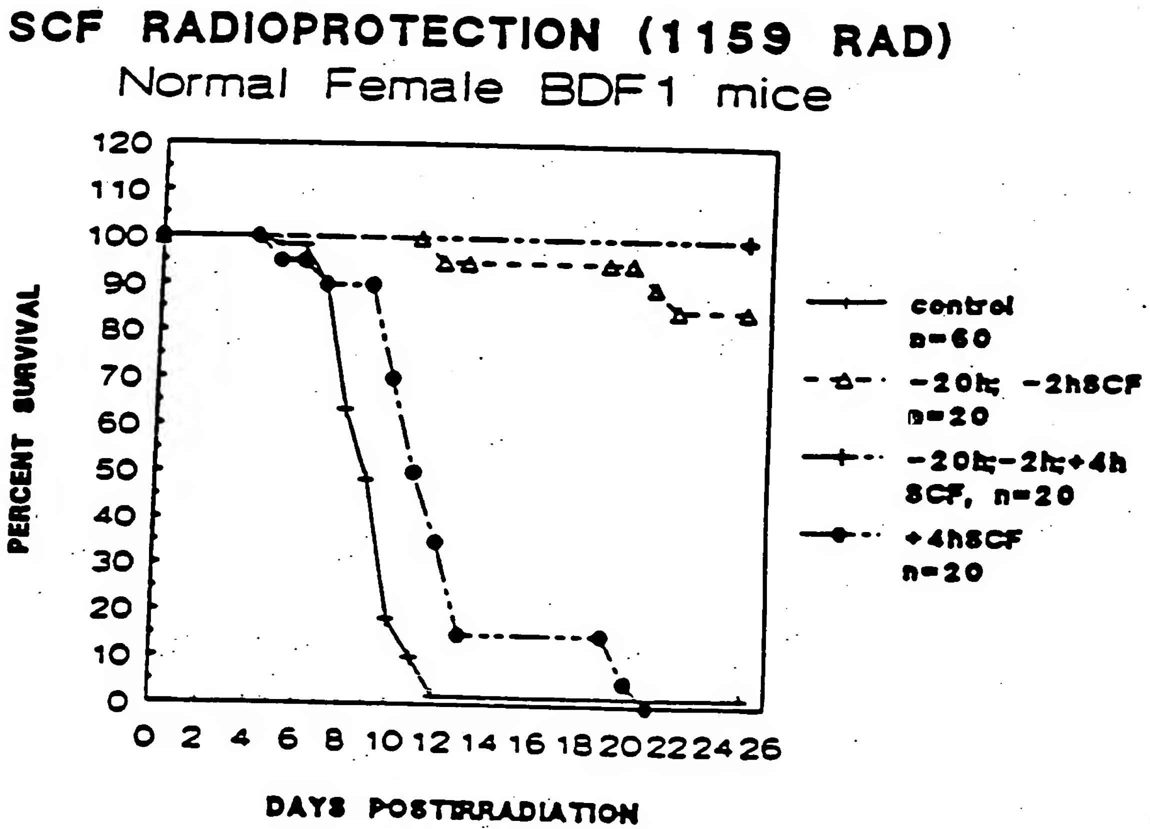

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26
DAYS POSTIRRADIATION
control
n=60
-20h; -2hSCF
n=20
-20h;-2h;+4h
SCF, n=20
+4hSCF
n=20

FIG. 50

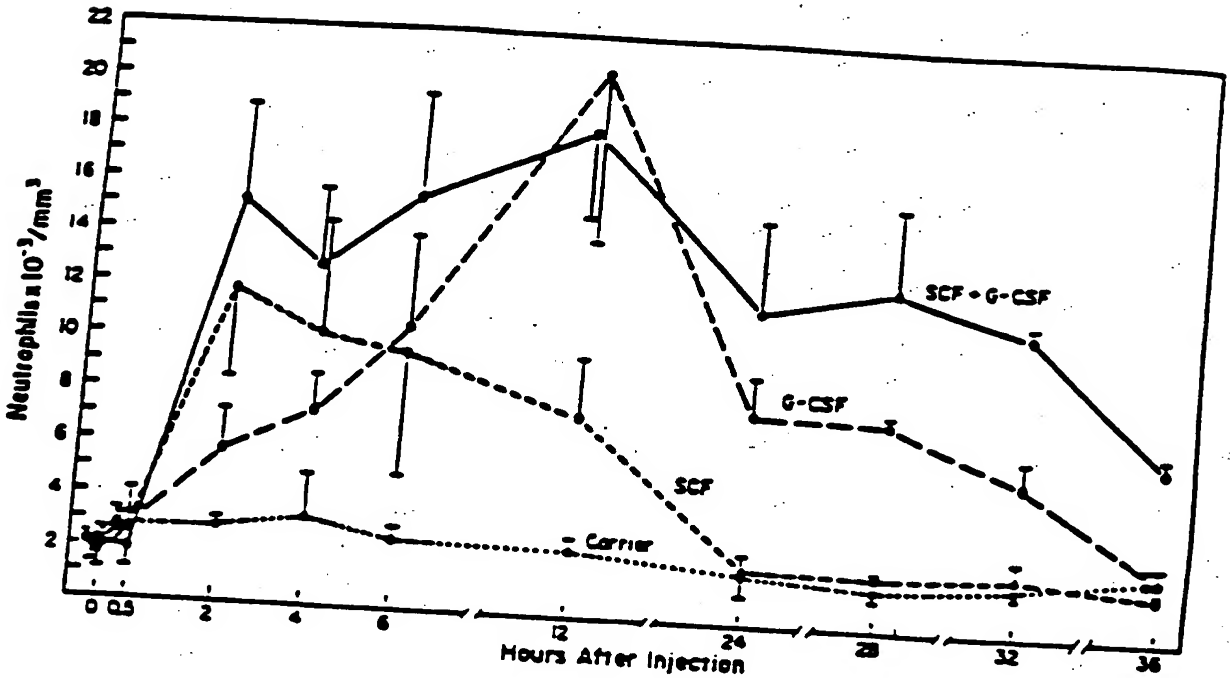

22
20
18
16
14
12
10
8
6
4
2
Neutrophils x 10⁻³/mm³
0
0.5
2
4
6
12
24
28
32
36
Hours After Injection
SCF + G-CSF
G-CSF
SCF
Carrier

FIG. 51

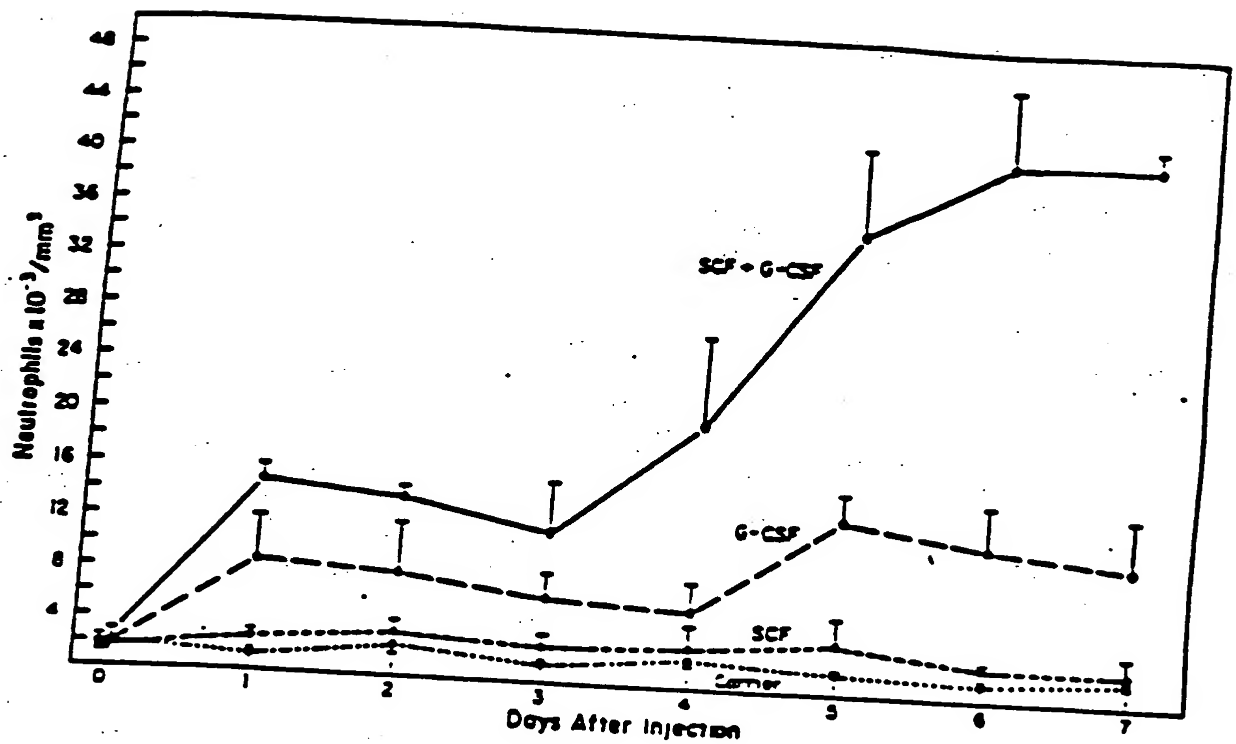

Neutrophils x 10^-3/mm^3
48
44
40
36
32
28
24
20
16
12
8
4
0
1
2
3
4
5
6
7
Days After Injection
SCF + G-CSF
G-CSF
SCF
Carrier

FIG. 52

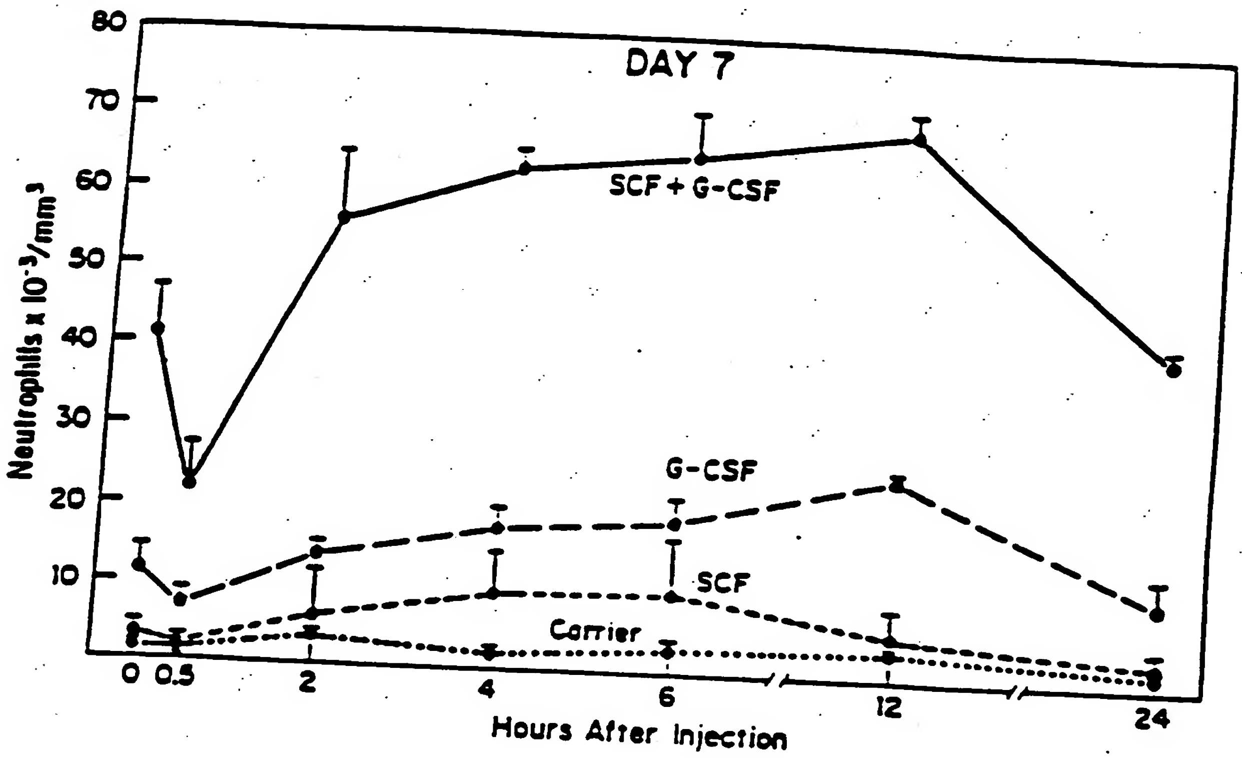

DAY 7
SCF + G-CSF
G-CSF
SCF
Carrier
Neutrophils x 10^{-3}/mm^3
80
70
60
50
40
30
20
10
0
0.5
2
4
6
12
24
Hours After Injection

FIG. 53

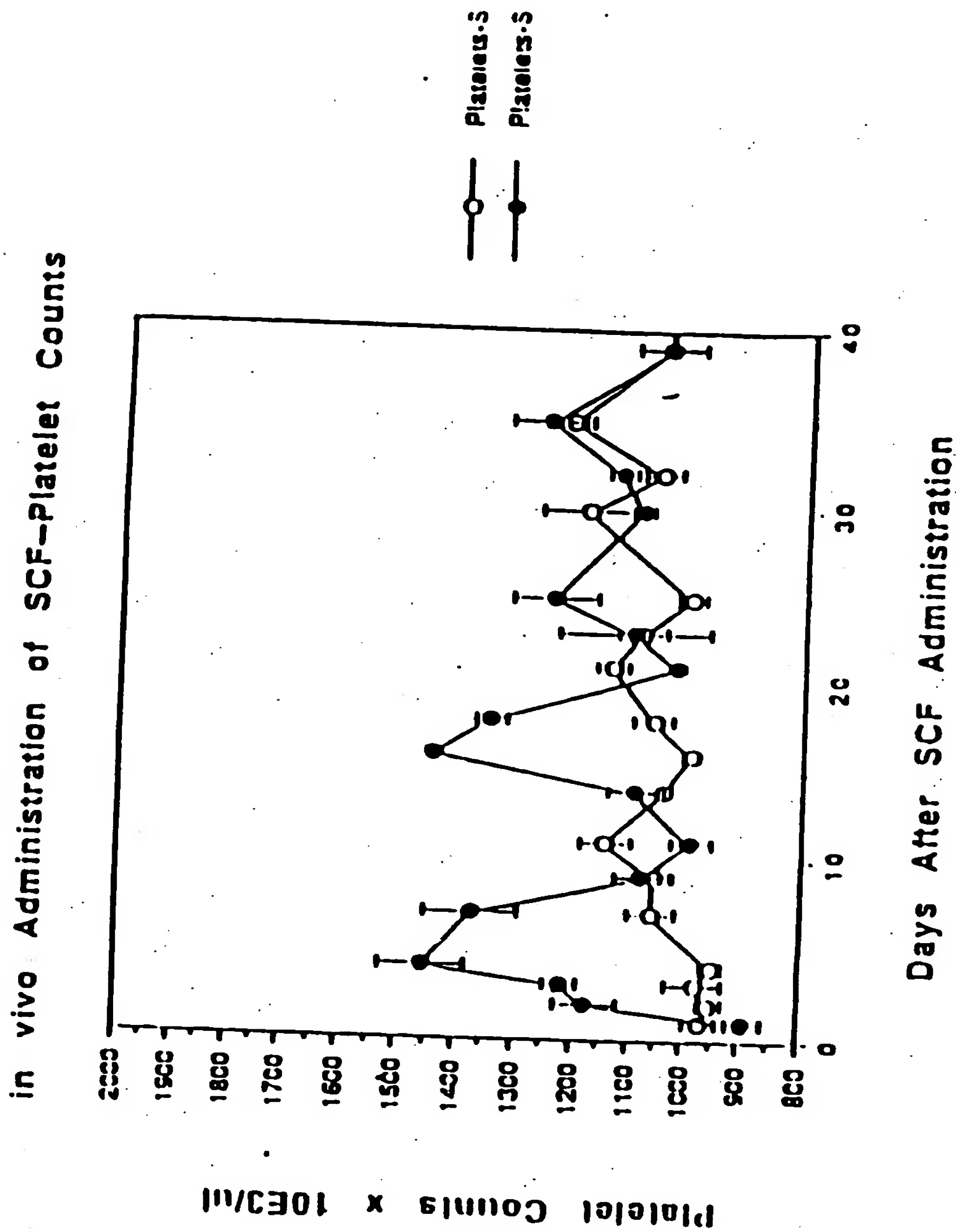

in vivo Administration of SCF–Platelet Counts
Platelet Counts x 10E3/ul
Days After SCF Administration
Platelets-S
Platelets-S
800
900
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
0
10
20
30
40

FIG. 54

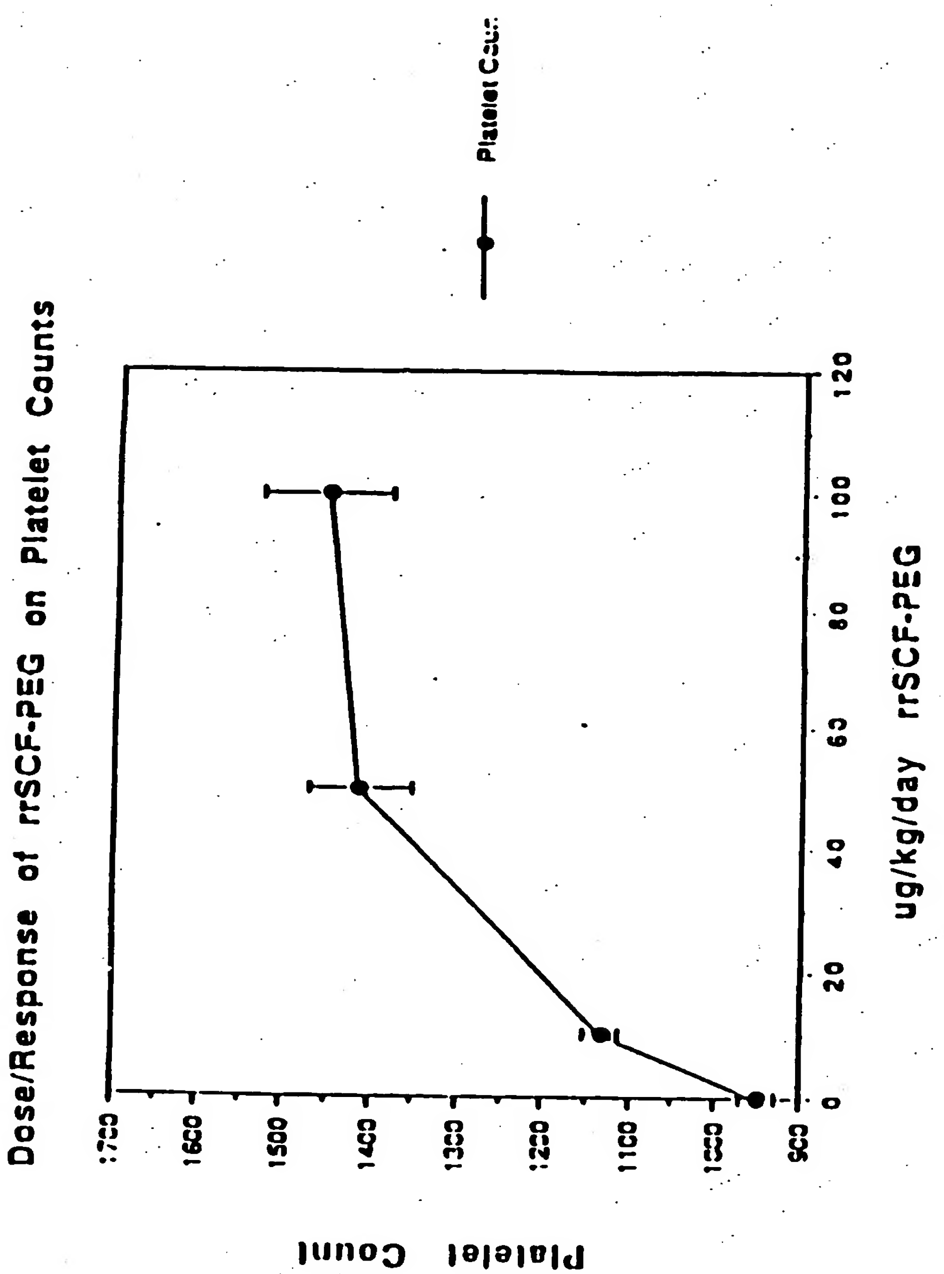

Dose/Response of rrSCF-PEG on Platelet Counts
Platelet Count
1700
1600
1500
1400
1300
1200
1100
1000
900
0
20
40
60
80
100
120
ug/kg/day rrSCF-PEG

FIG. 55

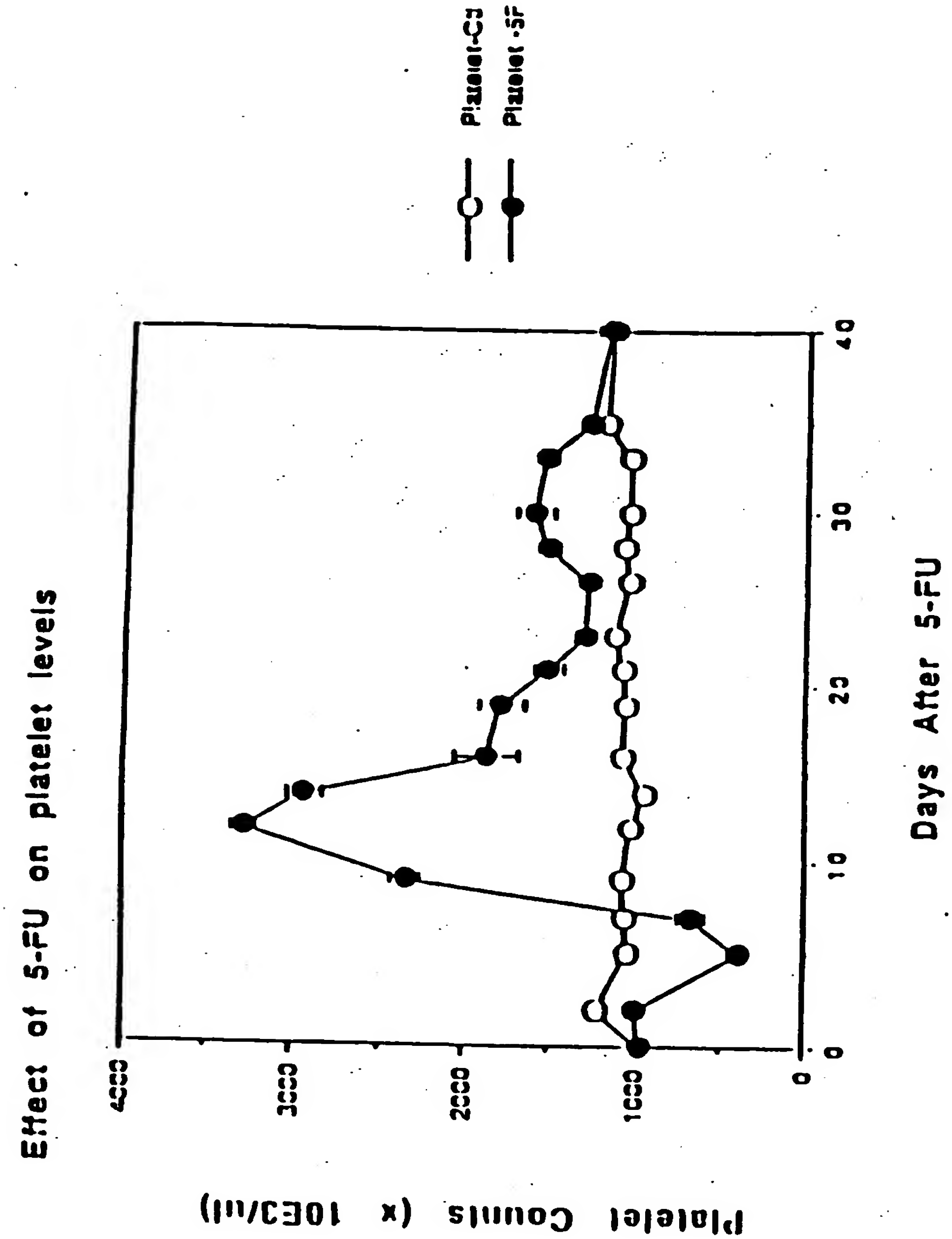
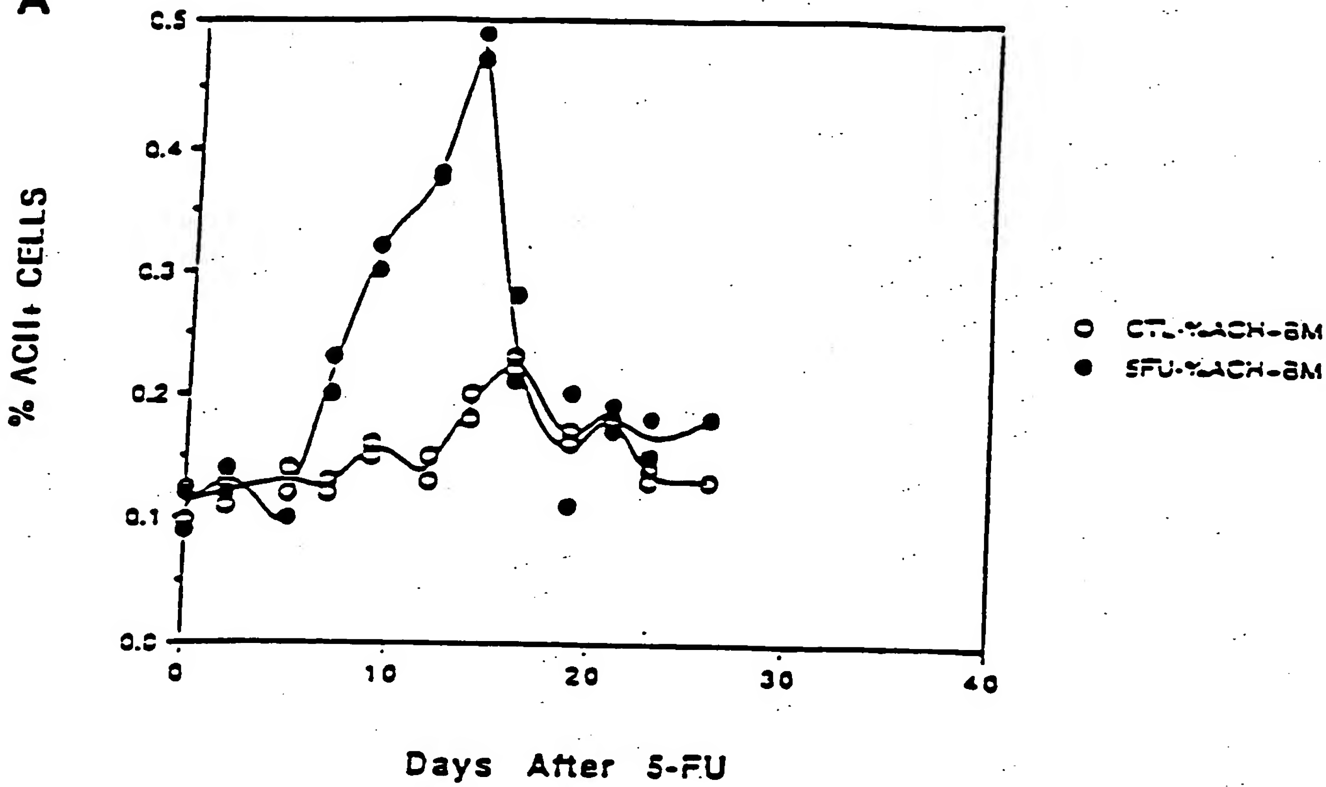

Effect of 5-FU on platelet levels
Platelet Counts (x 10E3/ul)
Days After 5-FU
0
1000
2000
3000
4000
0
10
20
30
40
Platelet -SF

FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

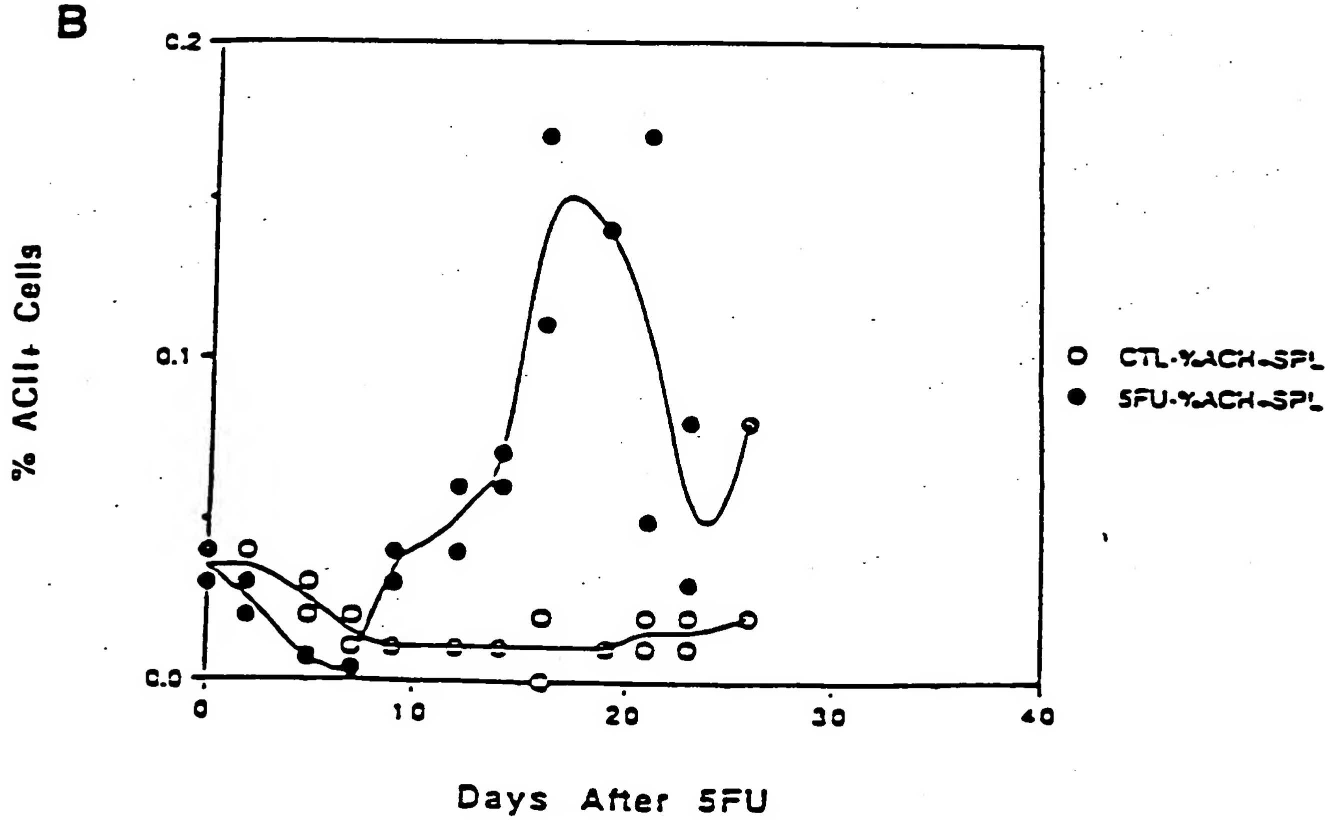


FIG. 57

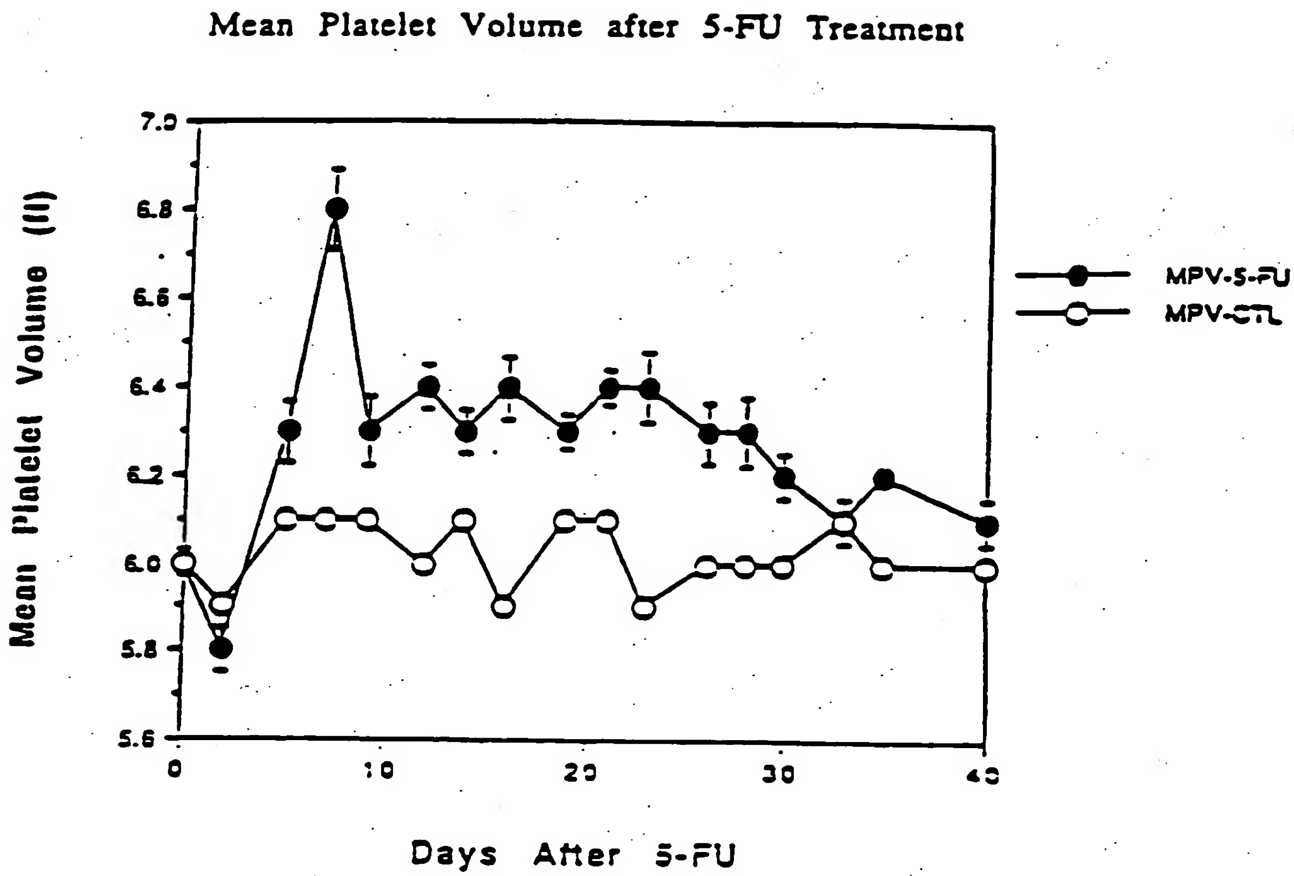

Mean Platelet Volume after 5-FU Treatment
Mean Platelet Volume (fl)
7.0
6.8
6.6
6.4
6.2
6.0
5.8
5.6
0
10
20
30
40
Days After 5-FU
MPV-5-FU
MPV-CTL

FIG. 58

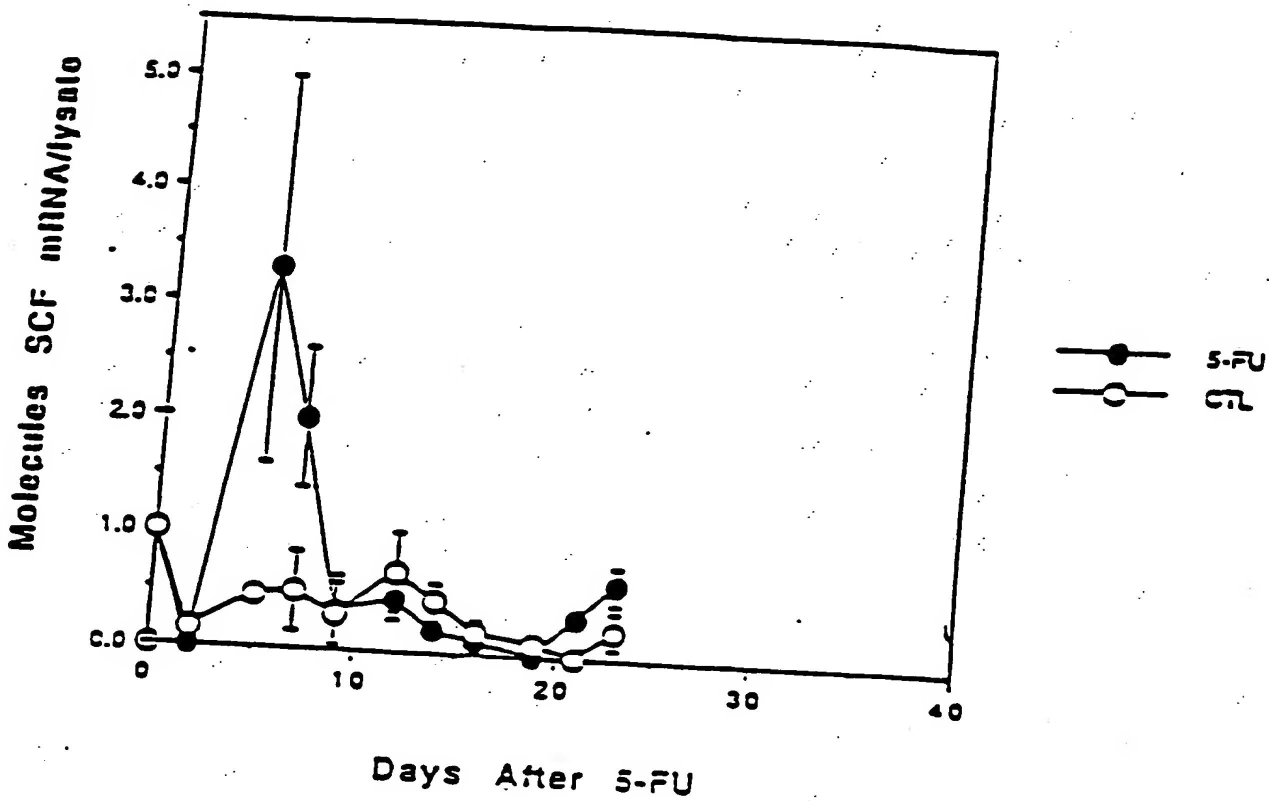

Molecules SCF mRNA/lysate
5.0
4.0
3.0
2.0
1.0
0.0
0
10
20
30
40
Days After 5-FU
5-FU
CTL

FIG. 59

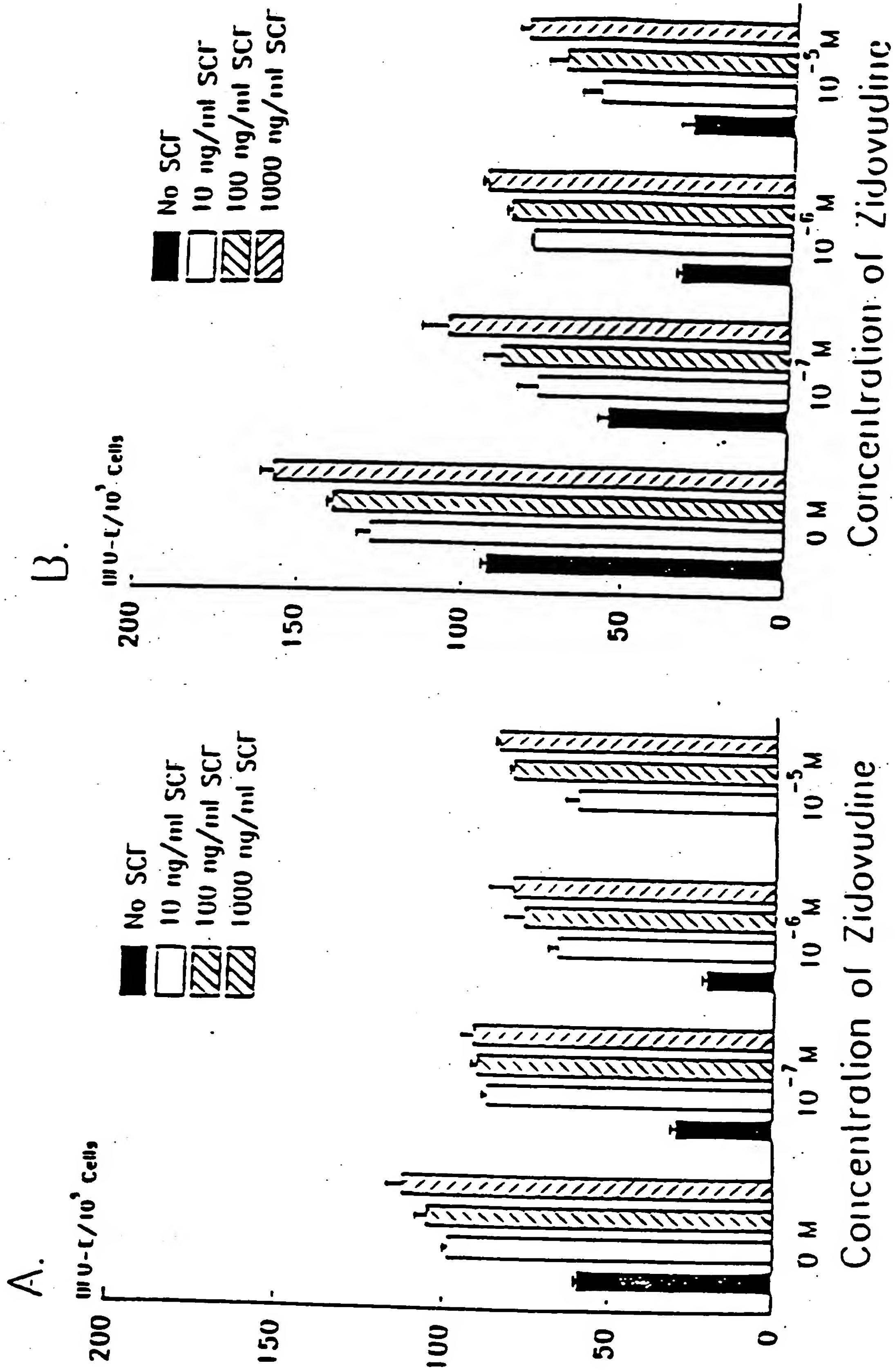

A.
B.
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0
50
100
150
200
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine

FIG. 60

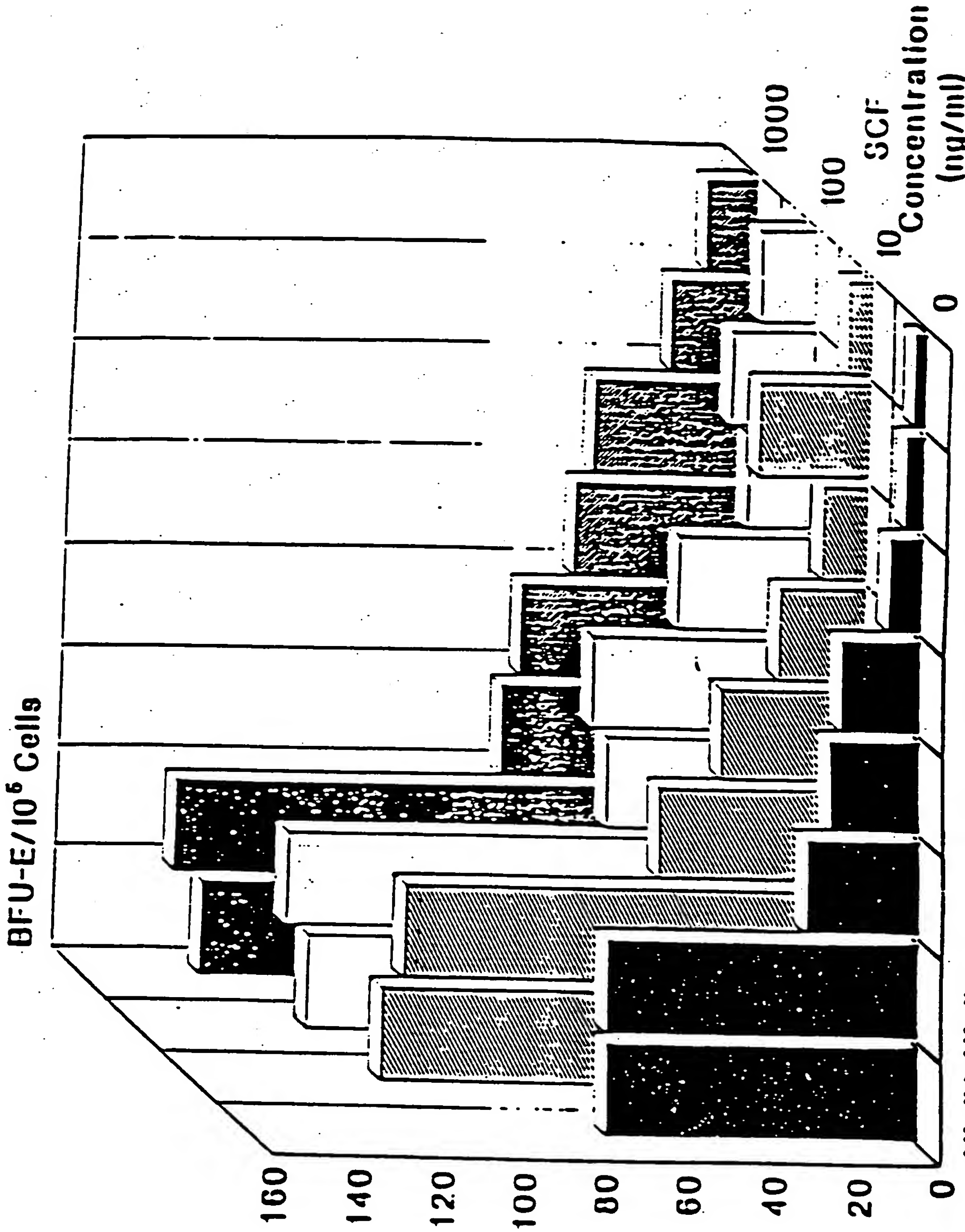

BFU-E/10^6 Cells
160
140
120
100
80
60
40
20
0
NL#1
NL#2
TG
PA
CW
AM
FS
SY
0
10
100
1000
SCF Concentration (ng/ml)

FIG. 61

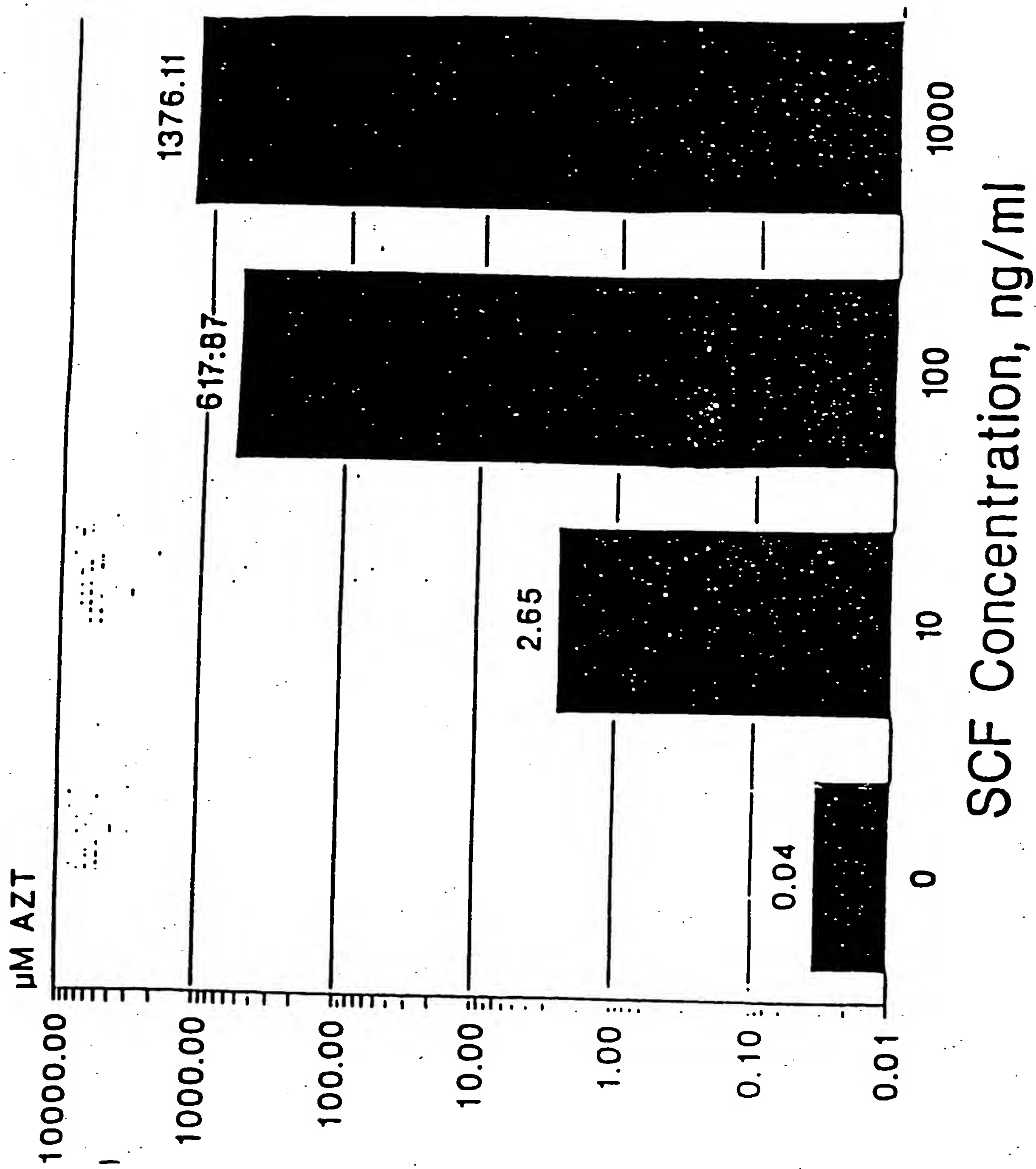

µM AZT
10000.00
1000.00
100.00
10.00
1.00
0.10
0.01
1376.11
617.87
2.65
0.04
0
10
100
1000
SCF Concentration, ng/ml

FIG. 62

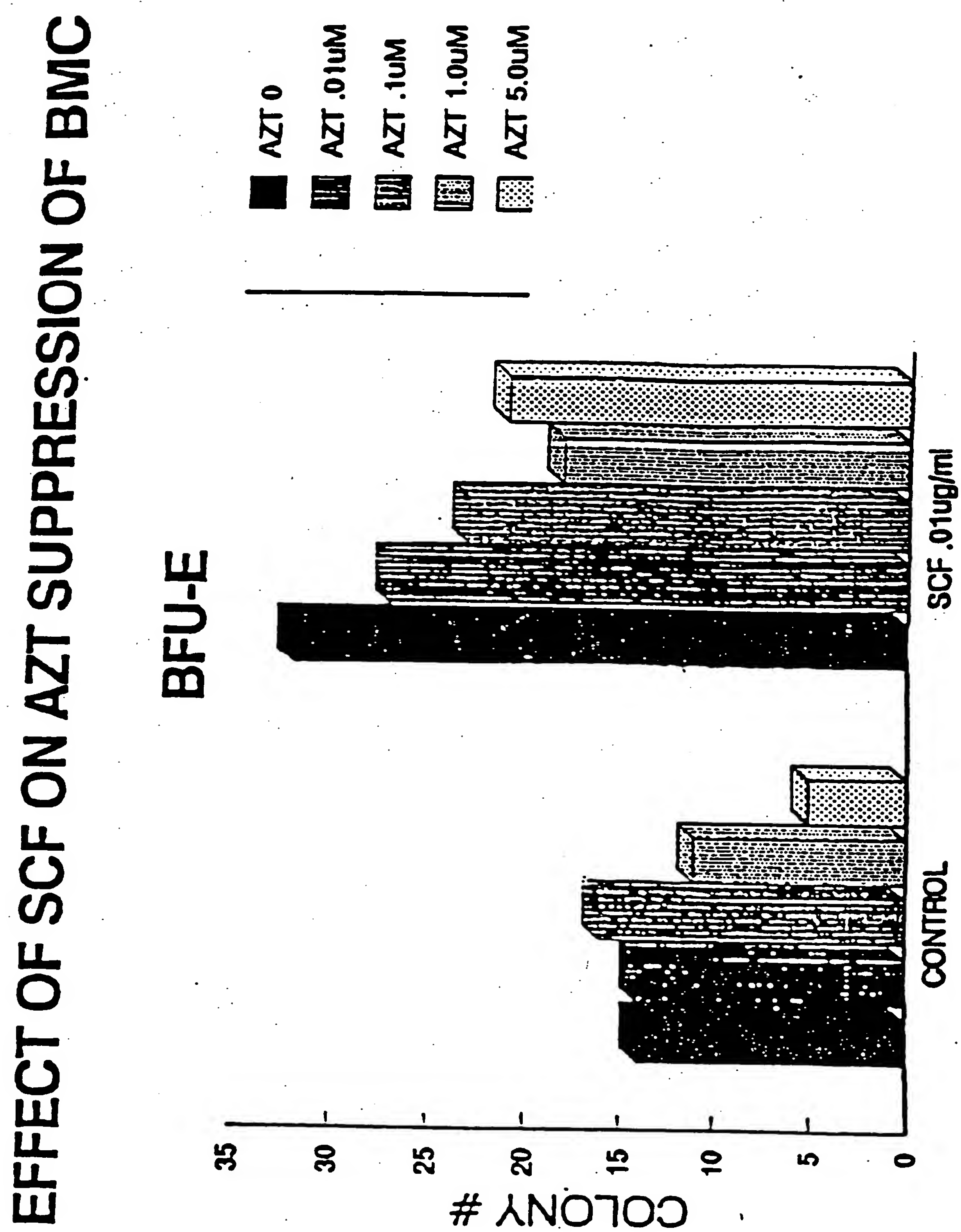

EFFECT OF SCF ON AZT SUPPRESSION OF BMC
BFU-E
AZT 0
AZT .01uM
AZT .1uM
AZT 1.0uM
AZT 5.0uM
COLONY #
0
5
10
15
20
25
30
35
CONTROL
SCF .01ug/ml

FIG. 63

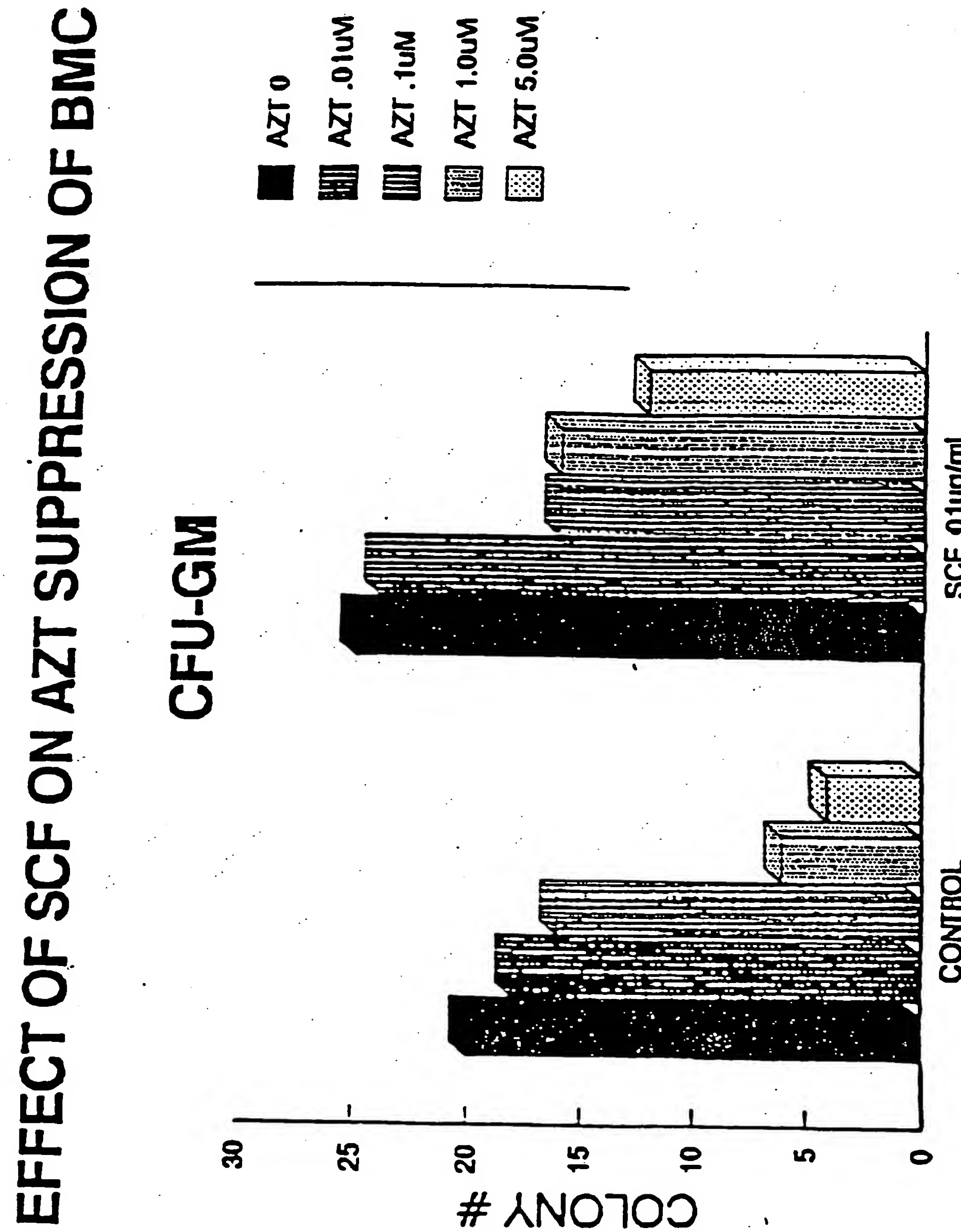

EFFECT OF SCF ON AZT SUPPRESSION OF BMC
CFU-GM
AZT 0
AZT .01uM
AZT .1uM
AZT 1.0uM
AZT 5.0uM
COLONY #
30
25
20
15
10
5
0
CONTROL
SCF .01ug/ml

FIG. 64

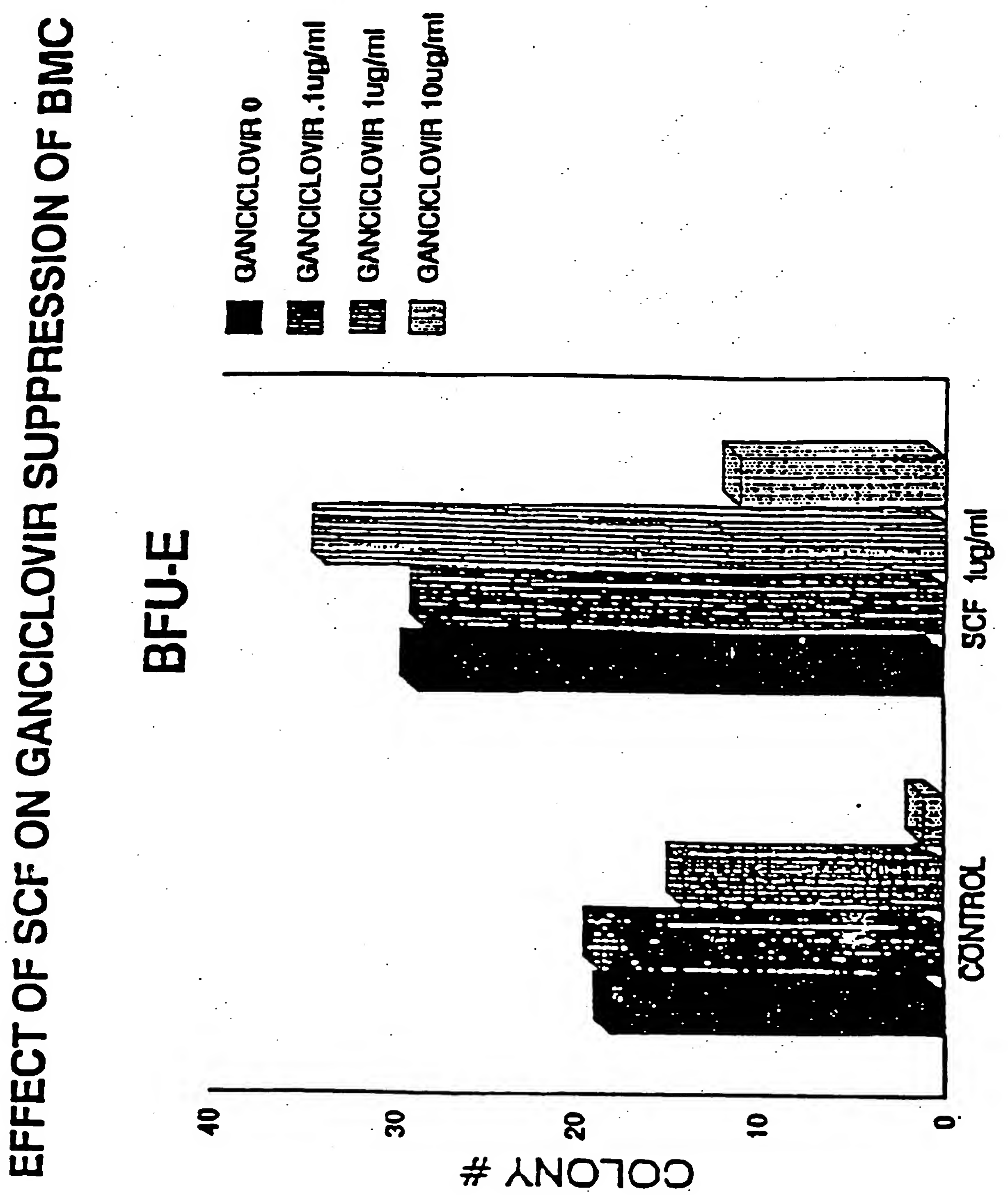

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC
BFU-E
GANCICLOVIR 0
GANCICLOVIR .1ug/ml
GANCICLOVIR 1ug/ml
GANCICLOVIR 10ug/ml
COLONY #
40
30
20
10
0
CONTROL
SCF 1ug/ml

FIG. 65

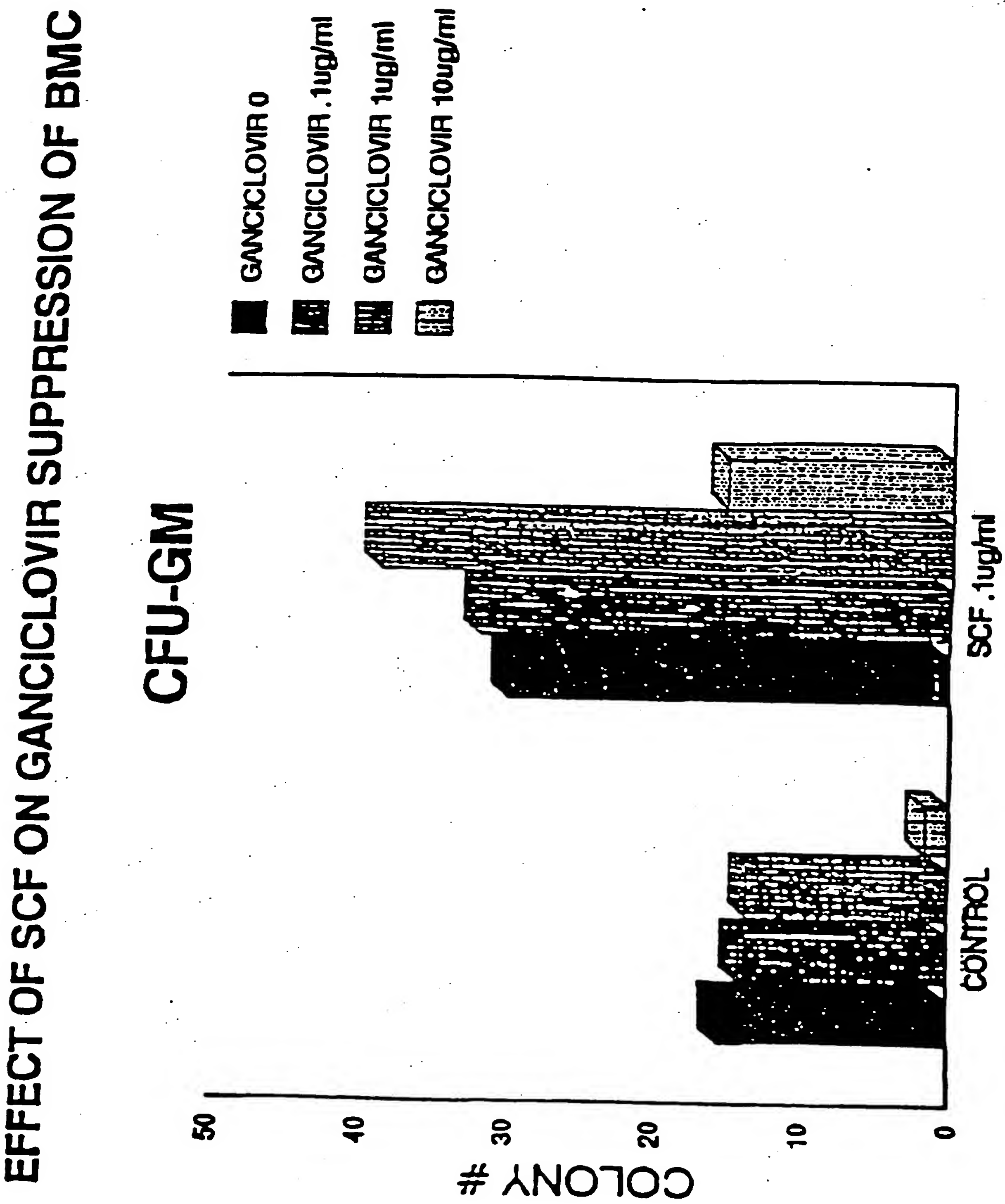

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC
CFU-GM
GANCICLOVIR 0
GANCICLOVIR .1ug/ml
GANCICLOVIR 1ug/ml
GANCICLOVIR 10ug/ml
COLONY #
0
10
20
30
40
50
CONTROL
SCF .1ug/ml

FIG. 66

Effects of SCF on CFU-S Number

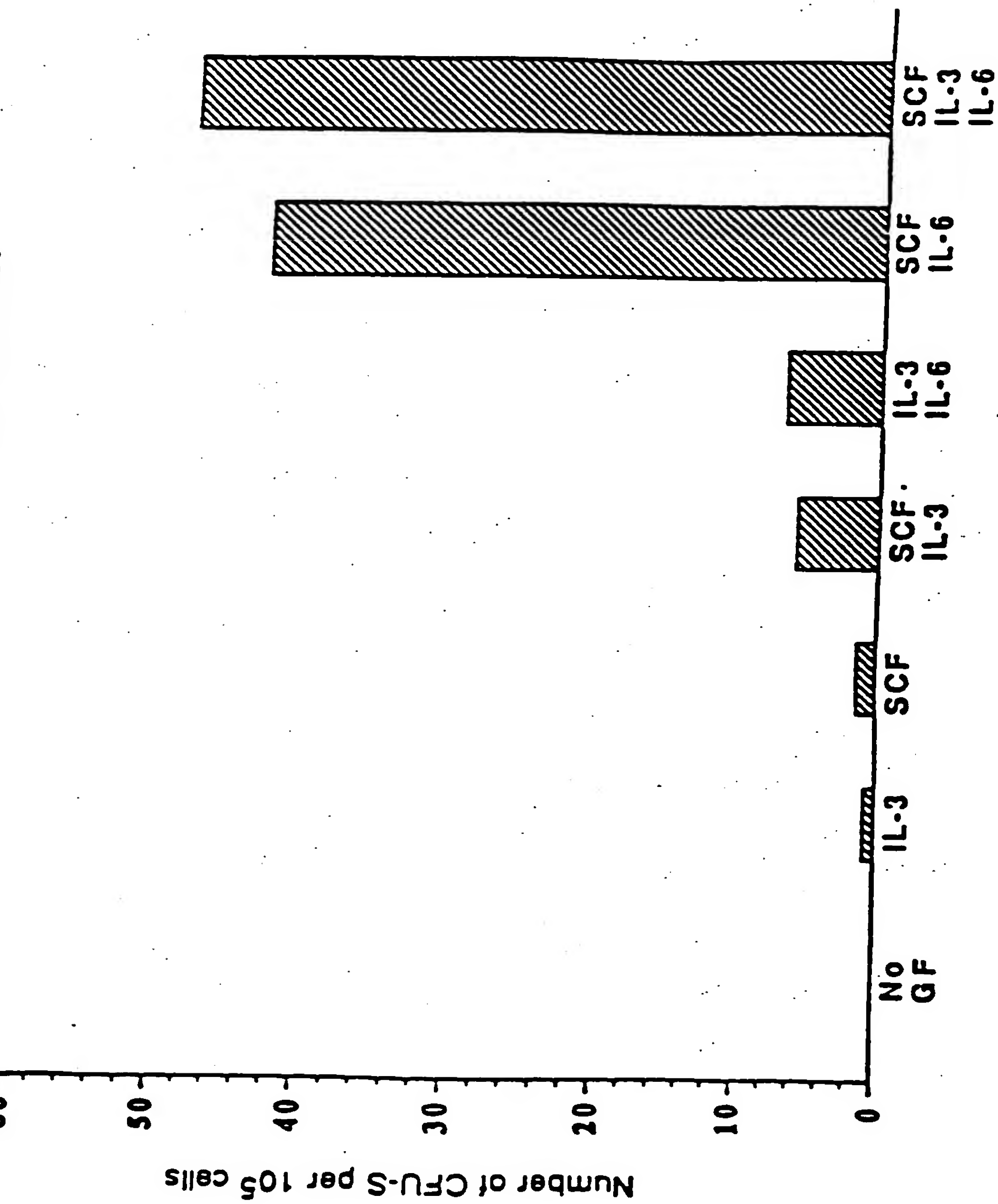


FIG. 67

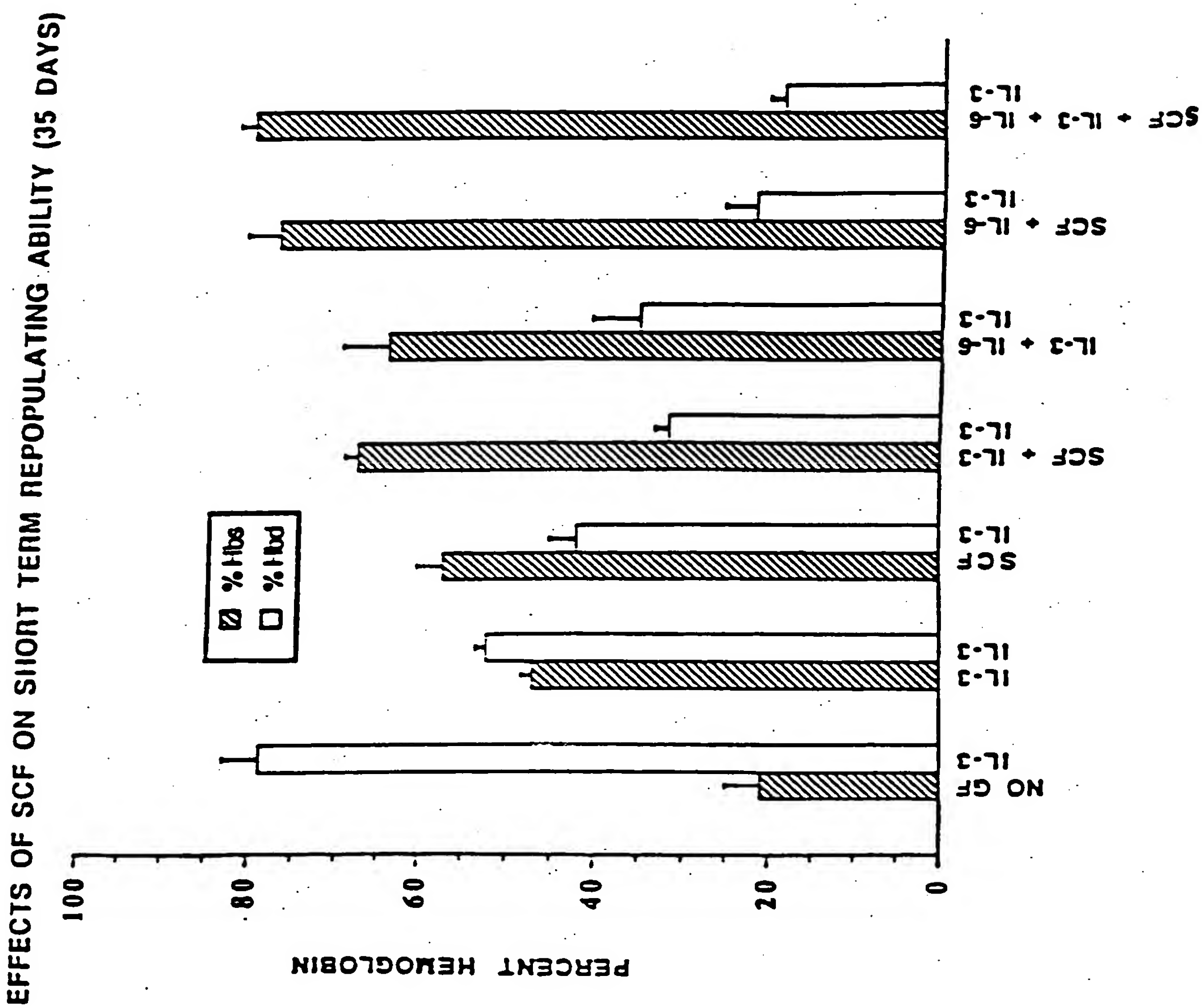

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)
PERCENT HEMOGLOBIN
0
20
40
60
80
100
% Hbs
% Hbd
NO GF
IL-3
IL-3
IL-3
SCF
IL-3
SCF + IL-3
IL-3
IL-3 + IL-6
IL-3
SCF + IL-6
IL-3
SCF + IL-3 + IL-6
IL-3

FIG. 68

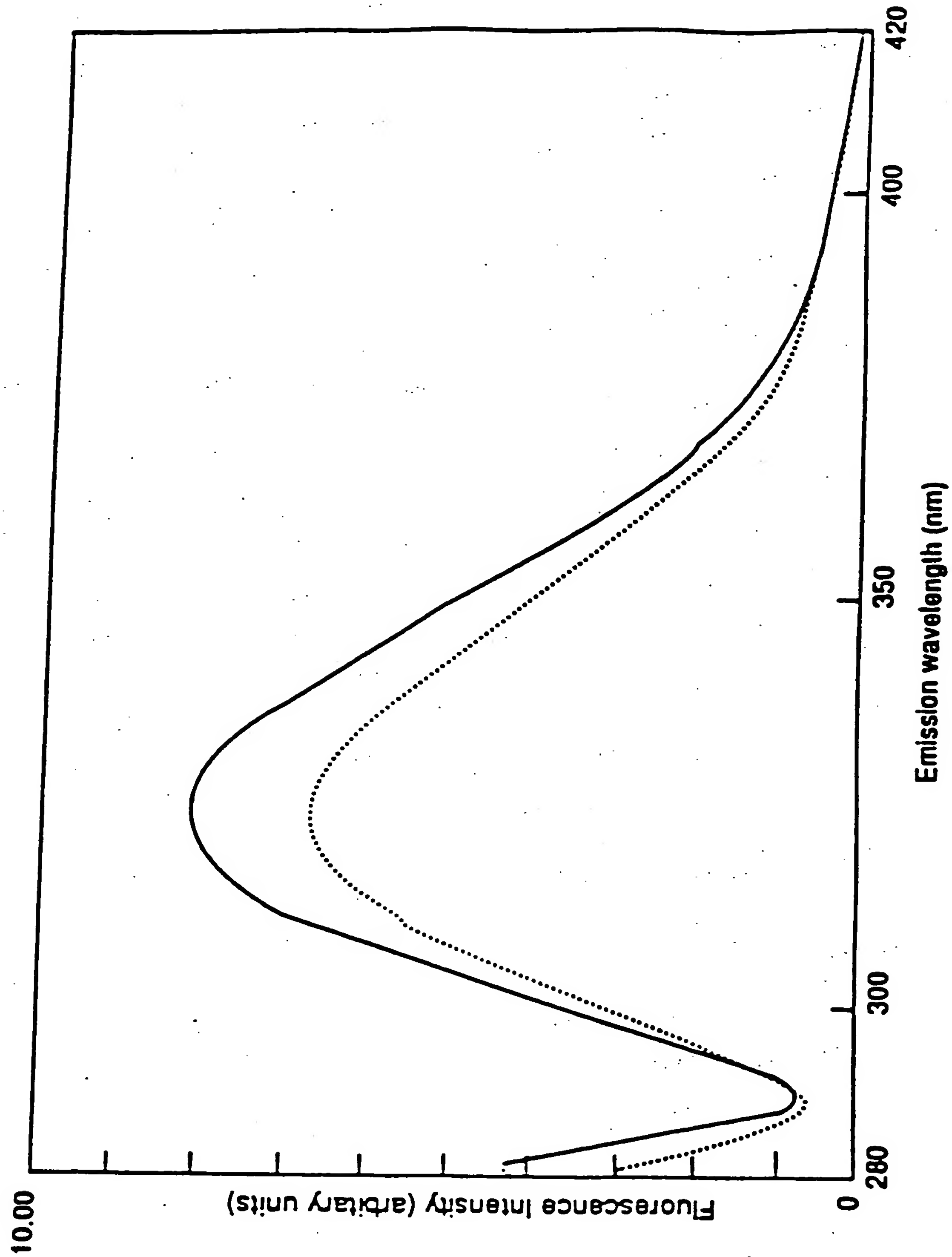

Fluorescence Intensity (arbitrary units)
10.00
0
280
300
350
400
420
Emission wavelength (nm)

FIG. 69A

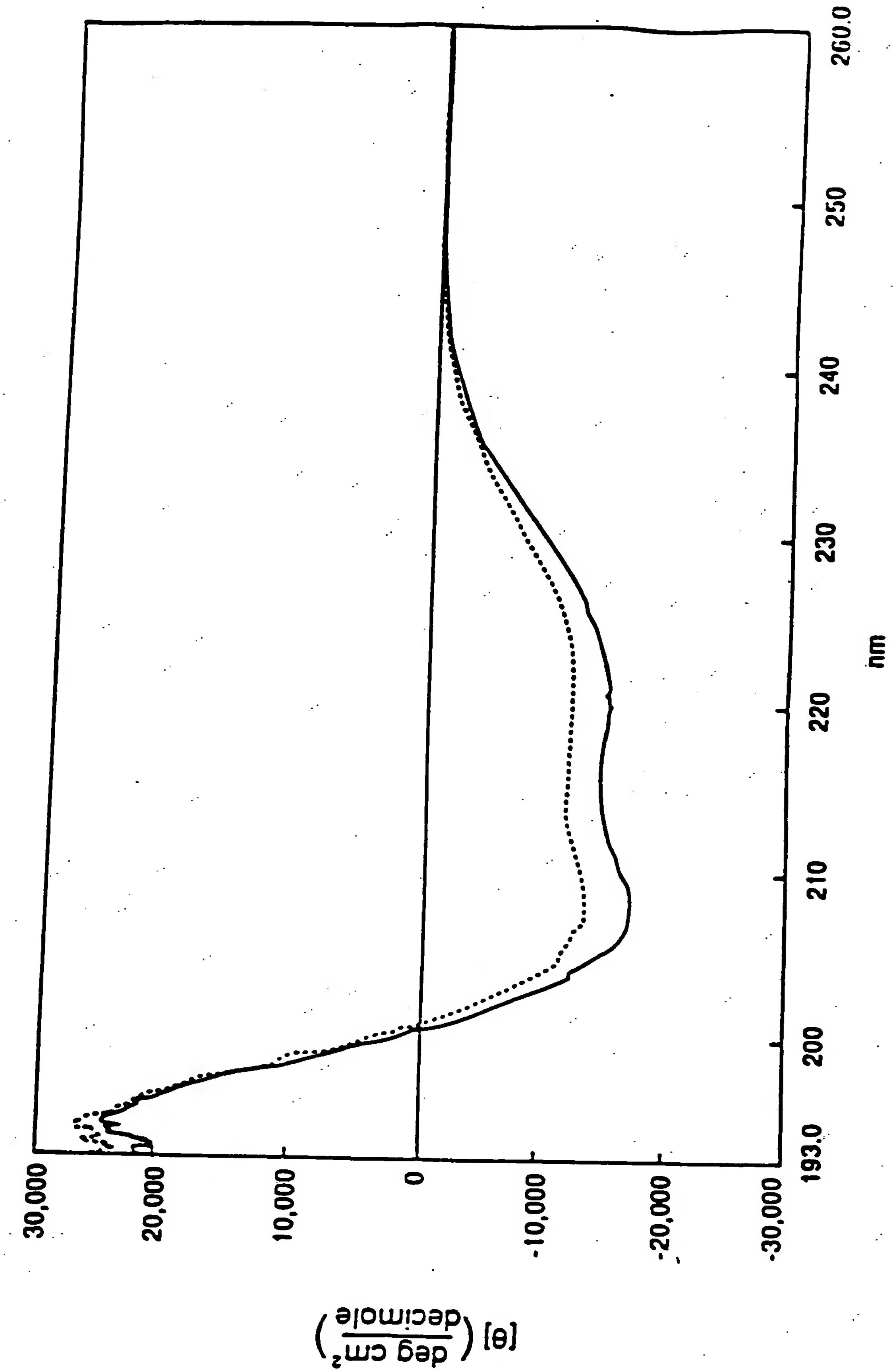

30,000
20,000
10,000
0
-10,000
-20,000
-30,000
[θ] (deg cm² / decimole)
193.0
200
210
220
230
240
250
260.0
nm

FIG. 69B

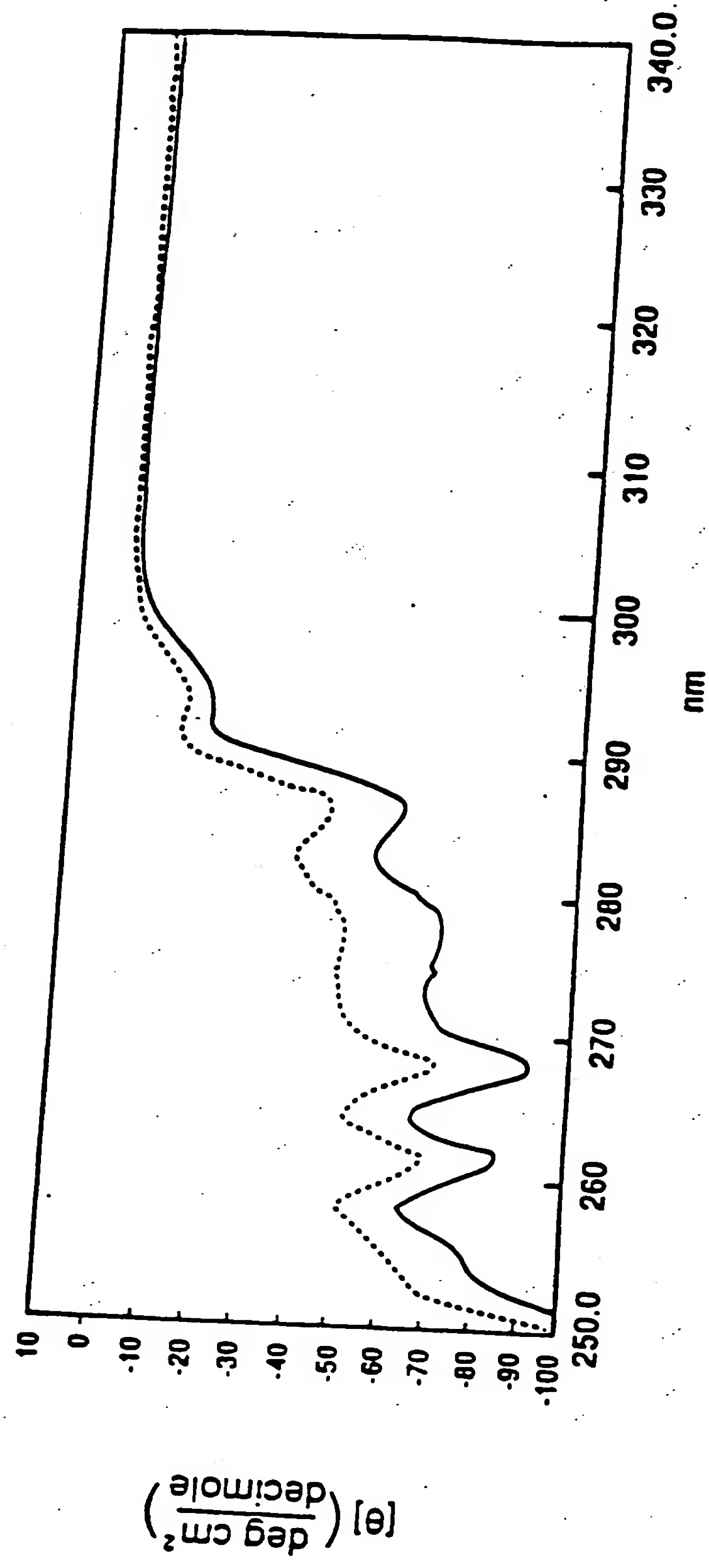

nm
250.0
260
270
280
290
300
310
320
330
340.0
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
[θ] (deg cm² / decimole)

FIG. 70